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OM protein - protein search, using sw model

Run on: January 4, 2005, 06:58:59 ; Search time 27 Seconds
(without alignments)
788,447 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 321
Sequence: 1 MGILLGLLGLHLYVDYGR.....AYIMLCRKTSQEHVYEAAR 321

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	4	US-09-254-465A-2
2	137	42.7	306	4	US-09-369-247-63
3	8	2.5	218	4	US-09-252-991A-19931
4	8	2.5	312	2	US-09-014-969-17
5	8	2.5	667	4	US-09-538-082-1307
6	8	2.5	710	4	US-09-252-991A-25375
7	8	2.5	855	2	US-08-938-365-3
8	8	2.5	867	2	US-08-938-365-2
9	8	2.5	954	2	US-08-749-169A-3
10	8	2.5	954	2	US-09-110-032A-3
11	8	2.5	954	4	US-09-866-028-7
12	8	2.5	954	4	US-09-944-457-7
13	8	2.5	955	4	US-09-798-051-8
14	8	2.2	20	2	US-08-078-311-9
15	7	2.2	20	2	US-08-460-402-9
16	7	2.2	24	3	US-08-957-001B-22
17	7	2.2	24	3	US-09-496-301-22
18	7	2.2	49	3	US-09-208-140-5
19	7	2.2	49	3	US-09-208-140-6
20	7	2.2	77	4	US-09-270-767-57911
21	7	2.2	100	4	US-09-134-000C-5929
22	7	2.2	110	4	US-09-248-796A-26879
23	7	2.2	116	1	US-08-053-131-185
24	7	2.2	116	2	US-08-096-762-185
25	7	2.2	117	3	US-09-042-353-48
26	7	2.2	117	3	US-08-758-417A-313
27	7	2.2	125	4	US-09-647-468-159

28	7	2.2	125	4	US-09-647-468-160	Sequence 160, App
29	7	2.2	128	1	US-08-259-372A-14	Sequence 14, Appl
30	7	2.2	128	1	US-08-468-671-14	Sequence 14, Appl
31	7	2.2	128	2	US-08-470-139-8	Sequence 8, Appl
32	7	2.2	128	3	US-09-347-061-8	Sequence 8, Appl
33	7	2.2	128	4	US-09-537-911A-68	Sequence 68, Appl
34	7	2.2	128	4	US-09-855-271-8	Sequence 8, Appl
35	7	2.2	129	1	US-08-217-918-2	Sequence 2, Appl
36	7	2.2	135	4	US-09-582-337-24	Sequence 20, Appl
37	7	2.2	137	4	US-09-582-337-24	Sequence 21, Appl
38	7	2.2	136	4	US-09-270-767-32237	Sequence 32237, A
39	7	2.2	156	4	US-09-328-352-6509	Sequence 6509, Ap
40	7	2.2	170	4	US-09-583-110-2699	Sequence 2699, Ap
41	7	2.2	174	4	US-09-245-764-8	Sequence 8, Appl
42	7	2.2	184	2	US-08-078-311-4	Sequence 4, Appl
43	7	2.2	184	2	US-08-460-402-4	Sequence 4, Appl
44	7	2.2	203	2	US-08-667-939A-20	Sequence 20, Appl
45	7	2.2	203	4	US-08-433-123-20	Sequence 20, Appl
46	7	2.2	215	2	US-08-667-939A-18	Sequence 18, Appl
47	7	2.2	215	4	US-08-433-123-18	Sequence 18, Appl
48	7	2.2	233	2	US-08-667-939A-5	Sequence 5, Appl
49	7	2.2	233	2	US-08-667-939A-6	Sequence 6, Appl
50	7	2.2	233	2	US-08-667-939A-7	Sequence 7, Appl
51	7	2.2	233	2	US-08-667-939A-8	Sequence 8, Appl
52	7	2.2	233	4	US-08-433-123-5	Sequence 5, Appl
53	7	2.2	233	4	US-08-433-123-6	Sequence 6, Appl
54	7	2.2	233	4	US-08-433-123-7	Sequence 7, Appl
55	7	2.2	233	4	US-08-433-123-8	Sequence 8, Appl
56	7	2.2	234	3	US-07-690-192-2	Sequence 2, Appl
57	7	2.2	234	3	US-08-487-550-2	Sequence 2, Appl
58	7	2.2	234	4	US-09-526-098-2	Sequence 2, Appl
59	7	2.2	234	4	US-09-740-002-24	Sequence 24, Appl
60	7	2.2	234	4	US-09-800-002-26	Sequence 26, Appl
61	7	2.2	234	4	US-09-383-916-2	Sequence 150, App
62	7	2.2	234	4	US-09-383-916-2	Sequence 150, App
63	7	2.2	235	3	US-08-812-586-16	Sequence 16, Appl
64	7	2.2	235	4	US-09-535-832A-17	Sequence 17, Appl
65	7	2.2	235	4	US-09-800-729-152	Sequence 152, App
66	7	2.2	236	1	US-08-157-101A-5	Sequence 5, Appl
67	7	2.2	236	3	US-08-487-550-10	Sequence 10, Appl
68	7	2.2	236	4	US-09-526-098-10	Sequence 10, Appl
69	7	2.2	236	4	US-09-383-916-10	Sequence 10, Appl
70	7	2.2	239	3	US-08-487-550-6	Sequence 6, Appl
71	7	2.2	239	4	US-09-526-098-6	Sequence 6, Appl
72	7	2.2	239	4	US-09-383-916-6	Sequence 6, Appl
73	7	2.2	240	4	US-09-252-991A-17600	Sequence 17600, A
74	7	2.2	241	2	US-07-916-098A-56	Sequence 56, Appl
75	7	2.2	241	4	US-09-489-039A-8330	Sequence 8330, Ap
76	7	2.2	254	2	US-08-667-939A-2	Sequence 2, Appl
77	7	2.2	254	2	US-08-667-939A-3	Sequence 3, Appl
78	7	2.2	254	2	US-08-667-939A-4	Sequence 4, Appl
79	7	2.2	254	2	US-08-667-939A-9	Sequence 9, Appl
80	7	2.2	254	4	US-08-433-123-2	Sequence 2, Appl
81	7	2.2	254	4	US-08-433-123-3	Sequence 3, Appl
82	7	2.2	254	4	US-08-433-123-4	Sequence 4, Appl
83	7	2.2	254	4	US-08-433-123-9	Sequence 9, Appl
84	7	2.2	256	4	US-09-107-532A-5758	Sequence 5758, Ap
85	7	2.2	284	2	US-08-078-311-14	Sequence 14, Appl
86	7	2.2	284	2	US-08-078-311-24	Sequence 24, Appl
87	7	2.2	284	2	US-08-460-402-14	Sequence 14, Appl
88	7	2.2	284	2	US-08-460-402-24	Sequence 24, Appl
89	7	2.2	288	4	US-09-134-000C-6445	Sequence 6445, Ap
90	7	2.2	290	4	US-09-540-236-2615	Sequence 2615, Ap
91	7	2.2	291	4	US-09-107-532A-5063	Sequence 5063, Ap
92	7	2.2	307	3	US-08-812-886-2	Sequence 2, Appl
93	7	2.2	307	4	US-09-535-832A-2	Sequence 2, Appl
94	7	2.2	345	4	US-09-457-066-43	Sequence 43, Appl
95	7	2.2	345	4	US-09-564-595D-35	Sequence 35, Appl
96	7	2.2	345	4	US-09-706-868-43	Sequence 43, Appl
97	7	2.2	345	4	US-08-823-033-4	Sequence 4, Appl
98	7	2.2	354	4	US-09-270-767-42600	Sequence 42600, A
99	7	2.2	356	4	US-09-107-532A-4245	Sequence 4245, Ap
100	7	2.2	372	1	US-07-865-878A-4	Sequence 4, Appl


```
RESULT 4
US-09-014-969-17
; Sequence 17, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-014-969-17

Query Match 2.5%; Score 8; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 ILGLILL 10
DB 231 ILGLILL 238

RESULT 5
US-09-538-092-1307
; Sequence 1307, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Joic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
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SOFTWARE: CuraPatSegFormatter Version 0.9
; SEQ ID NO 1307
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q13438
US-09-538-092-1307

Query Match 2.5%; Score 8; DB 4; Length 667;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 ILGLILLG 11
DB 10 ILGLILLG 17

RESULT 6
US-09-252-991A-25375
; Sequence 25375, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25375
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25375

Query Match 2.5%; Score 8; DB 4; Length 710;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 ILGLILLG 11
DB 534 ILGLILLG 541

RESULT 7
US-08-938-365-3
; Sequence 3, Application US/08938365
; Patent No. 5989909
; GENERAL INFORMATION:
; APPLICANT: Yang, Pan
; TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,365
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FILING DATE: 26-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-938-365-3

Query Match 2.5%; Score 8; DB 2; Length 855;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
DB 8 LIGLILIG 15

RESULT 8

US-08-938-365-2
Sequence 2, Application US/08938365
Patent No. 5983909
GENERAL INFORMATION:
APPLICANT: Yang, Pan
TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,365
FILING DATE: 26-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
FRAGMENT TYPE: internal
US-08-938-365-2

Query Match 2.5%; Score 8; DB 2; Length 867;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
DB 13 LIGLILIG 20

RESULT 9

US-08-749-169A-3
Sequence 3, Application US/08749169A
Patent No. 5846770
GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAVALLIE, Edward
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,169A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-749-169A-3

Query Match 2.5%; Score 8; DB 2; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILIG 11
DB 13 LIGLILIG 20

RESULT 10

US-09-130-032A-3
Sequence 3, Application US/09130032A
Patent No. 5986056
GENERAL INFORMATION:
APPLICANT: LAVALLIE, Edward
APPLICANT: RACIE, Lisa
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: HUMAN CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,032A
FILING DATE: August 4, 1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-130-032A-3

Query Match 2.5%; Score 8; DB 2; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 LGALLIG 11
Db 13 LGALLIG 20

RESULT 11
US-09-866-028-7
Sequence 7, Application US/09866028
Patent No. 6642360
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBR OF SEQ ID NOS: 120
SEQ ID NO 7
LENGTH: 954
TYPE: PRT
ORGANISM: Homo Sapien
US-09-866-028-7

Query Match 2.5%; Score 8; DB 4; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 4 LGALLIG 11
Db 13 LGALLIG 20

RESULT 12
US-09-944-457-7
Sequence 7, Application US/09944457
Patent No. 6734288
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,457
FILING DATE: 2001-09-26
Prior application data removed - consult PALM or file wrapper
NUMBR OF SEQ ID NOS: 120
SEQ ID NO 7
LENGTH: 954
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-457-7

PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 15, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. 6734288ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. 6734288ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 7
LENGTH: 954
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-457-7

Query Match 2.5%; Score 8; DB 4; Length 954;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLG 11
13 LGGLLLG 20

RESULT 13
US-09-798-051-8
Sequence 8, Application US/09798051
Patent No. 6632780
GENERAL INFORMATION:
APPLICANT: Zhang, Ke
APPLICANT: Cam, Linh
APPLICANT: Nakayama, Naoki
TITLE OF INVENTION: Chordin-like-2 Molecules and Uses Thereof
FILE REFERENCE: 01-005
CURRENT APPLICATION NUMBER: US/09/798,051
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 955
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-051-8

Query Match 2.5%; Score 8; DB 4; Length 955;

Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLG 11
13 LGGLLLG 20

RESULT 14
US-08-078-311-9
Sequence 9, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselsbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francois
APPLICANT: Souyri, Michele
APPLICANT: Tambourlin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchyt, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-078-311-9

Query Match 2.2%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
14 LGGLLL 20

RESULT 15
US-08-460-402-9
Sequence 9, Application US/08460402
Patent No. 5989833
GENERAL INFORMATION:

APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francois
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 598933west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.84US03
TELEPHONE: 612-332-5300
TELECOMMUNICATION INFORMATION:
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-402-9

Query Match 2.2%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
14 LIGLILL 20

Db 14 LIGLILL 20

RESULT 16
US-08-957-001B-22
Sequence 22, Application US/08957001B
Patent No. 6228621
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madalo, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,001B
FILING DATE: 23-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,592
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-957-001B-22

Query Match 2.2%; Score 7; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
9 LIGLILL 15

Db 9 LIGLILL 15

RESULT 17
US-09-496-301-22
Sequence 22, Application US/09496301
Patent No. 6248565
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Madalo, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,301
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,001
FILING DATE: 23-OCT-1997

```
/ APPLICATION NUMBER: US 60/029,592
/ FILING DATE: 23-OCT-1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: UPN-3303
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-496-301-22

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 9 LGGLLL 15

RESULT 18
US-09-208-140-5
/ Sequence 5, Application US/09208140
/ Patent No. 6228576
/ GENERAL INFORMATION:
/ APPLICANT: Del Vecchio, Alfred
/ TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
/ FILE REFERENCE: P50743
/ CURRENT APPLICATION NUMBER: US/09/208,140
/ CURRENT FILING DATE: 1998-12-09
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Viral
US-09-208-140-5

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 31 LGGLLL 37

RESULT 19
US-09-208-140-6
/ Sequence 6, Application US/09208140
/ Patent No. 6228576
/ GENERAL INFORMATION:
/ APPLICANT: Del Vecchio, Alfred
/ TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
/ FILE REFERENCE: P50743
/ CURRENT APPLICATION NUMBER: US/09/208,140
/ CURRENT FILING DATE: 1998-12-09
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Viral
US-09-208-140-6
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Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 31 LGGLLL 37

RESULT 20
US-09-270-767-57911
/ Sequence 57911, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentn Ver. 2.0
/ SEQ ID NO 57911
/ LENGTH: 77
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
/ FEATURE:
/ OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57911

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 ATLSTLL 197
   |||||
Db 5 ATLSTLL 11

RESULT 21
US-09-134-000C-5929
/ Sequence 5929, Application US/09134000C
/ Patent No. 6617156
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
/ FILE REFERENCE: 032796-032
/ CURRENT APPLICATION NUMBER: US/09/134,000C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/055,778
/ PRIOR FILING DATE: 1997-06-15
/ NUMBER OF SEQ ID NOS: 6812
/ SOFTWARE: Patentn version 3.1
/ SEQ ID NO 5929
/ LENGTH: 100
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
US-09-134-000C-5929

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 100;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
   |||||
Db 41 LGGLLL 47

RESULT 22
US-09-248-796A-26879
/ Sequence 26879, Application US/09248796A
/ Patent No. 6747137
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; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ. ID NOS: 28208
; SEQ ID NO 26879
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-26879

Query Match
Best Local Similarity 100.0%; Pred. No. 53; Length 110;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 250 PLKATST 256
Db 41 PLKATST 47

RESULT 23
; US-08-053-131-185
; Sequence 185, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; US-08-096-762-185
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-053-131-185

Query Match
Best Local Similarity 100.0%; Pred. No. 55; Length 116;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 LGLGLLL 10
Db 9 LGLGLLL 15

RESULT 24
; US-08-096-762-185
; Sequence 185, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-096-762-185

Query Match
Best Local Similarity 100.0%; Pred. No. 55; Length 116;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 25
US-09-042-353-48
Sequence 48, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-353-48

Query Match 2.2%; Score 7; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 9 LIGLILL 15

RESULT 26
US-08-758-417A-313
Sequence 313, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-08-758-417A-313

Query Match 2.2%; Score 7; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGLL 10
DB 9 LGLLGLL 15

RESULT 27
US-09-647-468-159
Sequence 159, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 159
LENGTH: 125
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for L chain V region of ant-TF
US-09-647-468-159

Query Match 2.2%; Score 7; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGLL 10
DB 5 LGLLGLL 11

RESULT 28
US-09-647-468-160
Sequence 160, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 160
LENGTH: 125
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for L chain V region of ant-TF
US-09-647-468-160

Query Match 2.2%; Score 7; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGLL 10
DB 5 LGLLGLL 11

RESULT 29
US-08-259-372A-14
Sequence 14, Application US/08259372A
Patent No. 5565354
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-372A-14

Query Match 2.2%; Score 7; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
Db 7 LGGLLL 13

RESULT 30
US-08-468-671-14
Sequence 14, Application US/08468671
Patent No. 5648077
GENERAL INFORMATION:
APPLICANT: Oseberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-671-14

Query Match 2.2%; Score 7; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
Db 7 LGGLLL 13

RESULT 31
US-08-470-139-8
Sequence 8, Application US/08470139
Patent No. 5998586
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-139-8

Query Match 2.2%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
Db 7 LGGLLL 13

RESULT 32
US-09-347-061-8
Sequence 8, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Achwal, Diljeet Singh
APPLICANT: Emage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 128
TYPE: PRT
ORGANISM: Rattus rattus
US-09-347-061-8

Query Match 2.2%; Score 7; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLGLL 10
Db 7 LGLGLL 13

RESULT 33
US-09-537-911A-68
Sequence 68, Application US/09537911A
Patent No. 6451982
GENERAL INFORMATION:
APPLICANT: Chou, Chuan-Chu
APPLICANT: Murgolo, Nicholas
APPLICANT: Abrams, John
APPLICANT: Jenh, Chung-her
APPLICANT: Petro, Mary
APPLICANT: Silver, Jon
APPLICANT: Tindall, Stephen
APPLICANT: Windsor, William
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Design, Cloning and Expression of Humanized Monoclonal Antibodies
TITLE OF INVENTION: Human Interleukin-5
FILE REFERENCE: JB0233KQ
CURRENT APPLICATION NUMBER: US/09/537,911A
CURRENT FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: 07/832,842
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: This antibody contains mouse and human sequences
US-09-537-911A-68

Query Match 2.2%; Score 7; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLGLL 10
Db 7 LGLGLL 13

RESULT 34
US-09-855-271-8
Sequence 8, Application US/09855271
Patent No. 6734286
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark W
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0088
CURRENT APPLICATION NUMBER: US/09/855,271
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/347,061
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1

SEQ ID NO 8
LENGTH: 128
TYPE: PRT
ORGANISM: Rattus rattus
US-09-855-271-8

Query Match 2.2%; Score 7; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLGLL 10
Db 7 LGLGLL 13

RESULT 35
US-08-217-918-2
Sequence 2, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-217-918-2

Query Match 2.2%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLGLL 10
Db 9 LGLGLL 15

RESULT 36
US-09-582-337-20
Sequence 20, Application US/09582337
Patent No. 6562618
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
TITLE OF INVENTION: and Medicinal Uses Thereof
FILE REFERENCE: JI-009PCT

```
/ CURRENT APPLICATION NUMBER: US/09/582,337
/ CURRENT FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: JP P1997-367699
/ PRIOR FILING DATE: 1997-12-25
/ PRIOR APPLICATION NUMBER: JP P1998-356183
/ PRIOR FILING DATE: 1998-12-15
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 135
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-582-337-20
```

```
Query Match          2.2%; Score 7; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 LAGLLLL 10
    |||||
Db 9 LAGLLLL 15
```

```
RESULT 37
US-09-582-337-24
/ Sequence 24, Application US/09582337
/ Patent No. 6562618
/ GENERAL INFORMATION:
/ APPLICANT: Japan Tobacco, Inc.
/ TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
/ FILE REFERENCE: J1-009PCT
/ CURRENT APPLICATION NUMBER: US/09/582,337
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: JP P1997-367699
/ PRIOR FILING DATE: 1997-12-25
/ PRIOR APPLICATION NUMBER: JP P1998-356183
/ PRIOR FILING DATE: 1998-12-15
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 24
/ LENGTH: 137
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-582-337-24
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```
Query Match          2.2%; Score 7; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 LAGLLLL 10
    |||||
Db 9 LAGLLLL 15
```

```
RESULT 38
US-09-270-767-32237
/ Sequence 32237, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ PRIOR FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 32237
/ LENGTH: 146
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-270-767-32237
```

```
Query Match          2.2%; Score 7; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 190 VATLSTL 196
    |||||
Db 105 VATLSTL 111
```

```
RESULT 39
US-09-328-352-6509
/ Sequence 6509, Application US/09328352
/ Patent No. 6562958
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Breton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
/ FILE REFERENCE: GTC99-03PA
/ CURRENT APPLICATION NUMBER: US/09/328,352
/ PRIOR FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 8252
/ SEQ ID NO 6509
/ LENGTH: 166
/ TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
US-09-328-352-6509
```

```
Query Match          2.2%; Score 7; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 229 VVKDSK 235
    |||||
Db 152 VVKDSK 158
```

```
RESULT 40
US-09-583-110-2699
/ Sequence 2699, Application US/09583110
/ Patent No. 6699703
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al.
/ TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
/ FILE REFERENCE: PATH00-07A
/ CURRENT APPLICATION NUMBER: US/09/583,110
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/107,433
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/085,131
/ PRIOR FILING DATE: 1998-05-12
/ PRIOR APPLICATION NUMBER: US 60/051,553
/ PRIOR FILING DATE: 1997-07-02
/ NUMBER OF SEQ ID NOS: 5322
/ SEQ ID NO 2699
/ LENGTH: 170
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-583-110-2699
```

```
Query Match          2.2%; Score 7; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 121 DGNQYR 127
    |||||
Db 87 DGNQYR 93
```

```
RESULT 41
US-09-245-764-8
/ Sequence 8, Application US/09245764
/ Patent No. 6675105
```

GENERAL INFORMATION:
APPLICANT: Hogarth, P. Mark
APPLICANT: Powell, Maree S.
APPLICANT: McKenzie, Ian P.C.
APPLICANT: Maxwell, Kelly F.
APPLICANT: Garrett, Thomas P.J.
APPLICANT: Epa, Vidana
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4102-4
CURRENT APPLICATION NUMBER: US/09/245,764
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/099,994
EARLIER FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: 60/073,972
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-09-245-764-8

Query Match 2.2%; Score 7; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 DSGSYFC 211
Db 148 DSGSYFC 154

RESULT 42
US-08-078-311-4
Sequence 4, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gisselbrecht, Sylvie
APPLICANT: Penciolelli, Jean-Francis
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-078-311-4

Query Match 2.2%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 59 LIGLILL 65

RESULT 43
US-08-460-402-4
Sequence 4, Application US/08460402
Patent No. 5989833
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gisselbrecht, Sylvie
APPLICANT: Penciolelli, Jean-Francis
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5989833west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.84US03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-402-4

Query Match 2.2%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLL 10
Db 59 LGLLL 65

RESULT 44
US-08-667-939A-20
Sequence 20, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-667-939A-20

Query Match 2.2%; Score 7; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 45
US-08-433-123-20
Sequence 20, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-123-20

Query Match 2.2%; Score 7; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 46
US-08-667-939A-18
Sequence 18, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUD, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUD-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-939A-18

Query Match 2.2%; Score 7; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 149 DSGSYFC 155

RESULT 47

US-08-433-123-18:
; Sequence 18, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LEO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LEO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-123-18

Query Match 2.2%; Score 7; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 149 DSGSYFC 155

RESULT 48

US-08-667-939A-5
; Sequence 5, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LEO, Shun

; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LEO=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-667-939A-5

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 49

US-08-667-939A-6
; Sequence 6, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LEO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUGO-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-6

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 50
US-08-667-939A-7
Sequence 7, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUGO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUGO-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-7

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 51
US-08-667-939A-8
Sequence 8, Application US/08667939A
Patent No. 5998166
GENERAL INFORMATION:
APPLICANT: LUGO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUGO-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-8

Query Match 2.2%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 52
US-08-433-123-5
Sequence 5, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LUGO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/433,123
FILING DATE: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-5

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 53
US-08-433-123-6
Sequence 6, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LWO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-6

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 54
US-08-433-123-7
Sequence 7, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LWO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-7

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 55
US-08-433-123-8
Sequence 8, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LWO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IJO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-8

Query Match 2.2%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
Db 166 DSGSYFC 172

RESULT 56
US-07-690-192-2
Sequence 2, Application US/07690192
Patent No. 5919650
GENERAL INFORMATION:
APPLICANT: Montano, Ximena
TITLE OF INVENTION: METHOD FOR INACTIVATION OF PROTEIN
TITLE OF INVENTION: FUNCTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,192
FILING DATE: 19910422
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bogden, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: DC13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-4163
TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-690-192-2

Query Match 2.2%; Score 7; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLGLLL 10
Db 7 LGLGLLL 13

RESULT 57
US-08-487-550-2
Sequence 2, Application US/08487550
Patent No. 613898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teaklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-2

Query Match 2.2%; Score 7; DB 3; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLGLLL 10
Db 7 LGLGLLL 13

RESULT 58
US-09-526-098-2
Sequence 2, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
US-09-526-098-2


```

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teeklin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-526-098-2
Query Match 2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGLL 10
Db 7 LGLLGLL 13

RESULT 59
US-09-740-002-24
; Sequence 24, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-24
Query Match 2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 LGLLGLL 10
Db 7 LGLLGLL 13

RESULT 60
US-09-740-002-26
; Sequence 26, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-26
Query Match 2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGLLGLL 10
Db 9 LGLLGLL 15

RESULT 61
US-09-800-729-150
; Sequence 150, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 150
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (120)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-150
Query Match 2.2%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 62
US-09-383-916-2
Sequence 2, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teakin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-2

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
|||||
Db 7 LGGLLL 13

RESULT 63
US-08-812-586-16
Sequence 16, Application US/08812586
Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Martin David, Tilson
TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53862-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-586-16

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
|||||
Db 9 LGGLLL 15

RESULT 64
US-09-535-832A-17
Sequence 17, Application US/09535832A
Patent No. 6537769
GENERAL INFORMATION:
APPLICANT: Tilson, Martin David
TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
FILE REFERENCE: 53862-AZ
CURRENT APPLICATION NUMBER: US/09/535,832A
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-535-832A-17

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
|||||
Db 9 LGGLLL 15

RESULT 65
US-09-800-729-152
Sequence 152, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIORITY APPLICATION NUMBER: PCT/US00/26013

PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 152
LENGTH: 235
TYPE: PR1
ORGANISM: Homo sapiens
US-09-800-729-152

Query Match 2.2%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGILL 10
| | | | |
DB 9 LIGILL 15

RESULT 66
US-08-157-101A-5
Sequence 5, Application US/08157101A
Patent No. 5808032
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIWA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBc ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437/204199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-157-101A-5

Query Match 2.2%; Score 7; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGILL 10
| | | | |
DB 9 LIGILL 15

RESULT 67
US-08-487-550-10
Sequence 10, Application US/08487550
Patent No. 613898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teekip, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-10

Query Match 2.2%; Score 7; DB 3; Length 236;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGILL 10
| | | | |
DB 7 LIGILL 13

RESULT 68
US-09-526-098-10
Sequence 10, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-10

Query Match 2.2%; Score 7; DB 4; Length 236;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 69
US-09-383-916-10
Sequence 10, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-10

Query Match 2.2%; Score 7; DB 4; Length 236;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 70
US-08-487-550-6
Sequence 6, Application US/08487550
Patent No. 613898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-6

Query Match 2.2%; Score 7; DB 3; Length 239;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
Db 7 LIGLILL 13

RESULT 71
US-09-526-098-6
Sequence 6, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teeklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-6

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 239;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLLL 10
Db 7 ILGLLL 13

RESULT 72
US-09-383-916-6
Sequence 6, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teeklin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-6

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 239;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLLL 10
Db 7 ILGLLL 13

RESULT 73
US-09-252-991A-17600
Sequence 17600, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17600
LENGTH: 240
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17600

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Length 240;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILGLLL 9
Db 48 ILGLLL 54

RESULT 74
US-07-916-098A-56
Sequence 56, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.

;; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;; NUMBER OF SEQUENCES: 61
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
;; STREET: 10 SOUTH WACKER DRIVE
;; CITY: CHICAGO
;; STATE: ILLINOIS
;; COUNTRY: U.S.A.
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORD PERFECT 5.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/916,098A
;; FILING DATE: July 24, 1992
;; CLASSIFICATION: 424
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/08843
;; FILING DATE: No. 5871732ember 27, 1991
;; CLASSIFICATION: 424
;; APPLICATION NUMBER: 07/618,542
;; FILING DATE: No. 5871732ember 27, 1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JOHN J. MC DONNELL
;; REGISTRATION NUMBER: 26,949
;; REFERENCE/DOCKET NUMBER: 92,310-G
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 715-1000
;; TELEFAX: (312) 715-1234
;;
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 241 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;;
;; MOLECULE TYPE: protein
;;
US-07-916-098A-56

Query Match 2.2%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||
DB 9 LIGLILL 15

RESULT 75

US-09-489-039A-8330
; Sequence 8330, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8330
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8330

Query Match 2.2%; Score 7; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LIGLILL 10
|||
DB 15 LIGLILL 21

Search completed: January 4, 2005, 07:00:03
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 06:58:59 ; Search time 115 seconds

(without alignments)
1606.046 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 321
Sequence: 1 MGILLGLLGLHGLTVDTYGR.....AYIMLCRKTSQEHVYEAAR 321

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : UniproC 02:*

1: uniproC_sprot:.*
2: uniproC_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	321	100.0	321	2	OGUX14
2	321	100.0	321	2	AAQ88707
3	321	100.0	321	2	Q9Y279
4	16	5.0	280	2	Q80WA3
5	16	5.0	280	2	BAC30780
6	9	2.8	178	2	Q72L88
7	9	2.8	178	2	AA880489
8	8	2.5	124	1	WFD2_CANFA
9	8	2.5	142	2	Q7ME51
10	8	2.5	217	2	Q8PI21
11	8	2.5	222	2	Q8ENJ3
12	8	2.5	223	2	Q91JY1
13	8	2.5	240	1	MTRA_METRA
14	8	2.5	240	1	MTRA_METRA
15	8	2.5	240	1	MTRA_METRA
16	8	2.5	249	2	Q6XPU4
17	8	2.5	249	2	AAAP4530
18	8	2.5	265	2	Q66648
19	8	2.5	265	2	Q95KP8
20	8	2.5	269	2	Q95KP9
21	8	2.5	271	2	Q95KQ0
22	8	2.5	292	2	Q6SFH9
23	8	2.5	292	2	AA38238
24	8	2.5	346	2	Q702H2
25	8	2.5	346	2	CAE28454
26	8	2.5	350	2	Q9GJ33
27	8	2.5	366	2	Q6TUV6
28	8	2.5	366	2	AA07413
29	8	2.5	412	2	Q30187
30	8	2.5	520	1	PSL2_HUMAN
31	8	2.5	537	2	Q7QIR0

32	8	2.5	590	2	Q6BSF5	Q6BSF5
33	8	2.5	595	1	STIL_HUMAN	Q96PQ1 homo sapien
34	8	2.5	597	1	STIL_PANTR	Q95101 pan troglod
35	8	2.5	612	2	Q6IBL2	Q6IB12 homo sapien
36	8	2.5	612	2	Q9BM99	Q9BM99 homo sapien
37	8	2.5	612	2	CAG33072	CAG33072 homo sapien
38	8	2.5	655	2	Q6JH13	Q6JH13 babesia bov
39	8	2.5	655	2	AA58046	AA58046 babesia b
40	8	2.5	667	1	Q59_HUMAN	Q59_HUMAN
41	8	2.5	750	2	Q72TS9	Q72TS9
42	8	2.5	752	2	AA669549	AA669549 leptospira
43	8	2.5	752	2	Q8FLE6	Q8FLE6 leptospira
44	8	2.5	937	2	Q86AH2	Q86AH2 dictyosteli
45	8	2.5	948	1	CHRD_MOUSE	Q92062 mus musculu
46	8	2.5	954	2	Q6UW63	Q6UW63 homo sapien
47	8	2.5	954	2	AAQ89285	AAQ89285 homo sapi
48	8	2.5	955	1	CHRD_HUMAN	Q9H2X0 homo sapien
49	8	2.5	975	2	Q86G86	Q86G86 pseudoplusi
50	8	2.2	20	1	CPBX_CAVPO	P34033 cavia porce
51	8	2.2	31	2	Q9QVA5	Q9QVA5 cavia (guin
52	8	2.2	33	2	Q9QV4	Q9QV4 cavia (guin
53	8	2.2	41	2	Q9QVY1	Q9QVY1 cavia (guin
54	8	2.2	42	2	Q70BW1	Q70BW1 sus scrofa
55	8	2.2	42	2	Q70BW2	Q70BW2 sus scrofa
56	8	2.2	42	2	CAE52546	CAE52546 sus scrof
57	8	2.2	42	2	CAE52547	CAE52547 sus scrof
58	8	2.2	44	2	Q9UN20	Q9UN20 homo sapien
59	8	2.2	66	2	Q8U2N4	Q8U2N4 pyrococcus
60	8	2.2	70	2	Q72H08	Q72H08 thermus t
61	8	2.2	70	2	AA582029	AA582029 thermus t
62	8	2.2	77	2	Q8TEA2	Q8TEA2 homo sapien
63	8	2.2	85	2	Q7UJ23	Q7UJ23 rhodospirill
64	8	2.2	88	2	Q8FEV3	Q8FEV3 escherichia
65	8	2.2	92	2	Q8KAN9	Q8KAN9 mus musculu
66	8	2.2	95	2	Q83JU5	Q83JU5 enterococcu
67	8	2.2	97	2	Q16755	Q16755 homo sapien
68	8	2.2	97	2	Q8GX66	Q8GX66 arabidopsis
69	8	2.2	98	2	Q950U7	Q950U7 rhizophyali
70	8	2.2	100	2	Q8Q555	Q8Q555 gallus galli
71	8	2.2	101	1	YGVA_YEAST	P53089 saccharomyc
72	8	2.2	101	2	AA566831	AA566831 saccharom
73	8	2.2	105	1	PLF4_RAT	P06765 rattus norv
74	8	2.2	105	2	Q70HT8	Q70HT8 mycoplasma
75	8	2.2	105	2	CAE45730	CAE45730 mycoplasma
76	8	2.2	105	2	CAE45731	CAE45731 mycoplasma
77	8	2.2	111	2	Q8LMS8	Q8LMS8 oryza sativ
78	8	2.2	117	1	KV11_HUMAN	P01601 homo sapien
79	8	2.2	117	2	KV1J_HUMAN	P01602 homo sapien
80	8	2.2	118	2	Q70HT1	Q70HT1 mycoplasma
81	8	2.2	118	2	Q70HT4	Q70HT4 mycoplasma
82	8	2.2	118	2	CAE45735	CAE45735 mycoplasma
83	8	2.2	118	2	CAE45736	CAE45736 mycoplasma
84	8	2.2	118	2	CAE45738	CAE45738 mycoplasma
85	8	2.2	119	2	Q6USA7	Q6USA7 saccharum h
86	8	2.2	119	2	AAQ95639	AAQ95639 saccharum
87	8	2.2	121	2	Q8CR98	Q8CR98 brachylococ
88	8	2.2	123	1	WFD2_RABIT	Q86R31 oryctolagus
89	8	2.2	126	2	Q67392	Q67392 aquilex aeo
90	8	2.2	127	2	Q9AGW6	Q9AGW6 nostoc punc
91	8	2.2	127	2	Q80Z00	Q80Z00 mus musculu
92	8	2.2	127	2	Q9DAK7	Q9DAK7 mus musculu
93	8	2.2	128	2	Q8C355	Q8C355 mus musculu
94	8	2.2	129	1	KV1W_HUMAN	P04433 homo sapien
95	8	2.2	129	1	KV1X_HUMAN	P04433 homo sapien
96	8	2.2	130	2	Q89U61	Q89U61 bradyrhizob
97	8	2.2	133	2	Q84BX3	Q84BX3 mycoplasma
98	8	2.2	138	2	Q73UT4	Q73UT4 mycobacteri
99	8	2.2	138	2	AA805820	AA805820 mycobacte
100	8	2.2	139	2	Q72IU6	Q72IU6 thermus the

ALIGNMENTS

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RESULT 1
OGX14 PRELIMINARY; PRT; 321 AA.
ID OGX14
AC OGX14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE STIGMA.
GN STIGMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22867236; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehnagiri S., Simons L., Singh J., Smith V., Stinson J., Vagtes A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358341; AAQ8707.1; -.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
SQ
SEQUENCE 321 AA; 35544 MW; B2AB2E3151D39C6E CRC64;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLGLHTVDTYGRPILEVPESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
DB 1 MGILLGLLGLHTVDTYGRPILEVPESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
QY 1 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
DB 1 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
QY 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
DB 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGSTSGAPGKSLPVFAIIILISLCMVFT 300
DB 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGSTSGAPGKSLPVFAIIILISLCMVFT 300
QY 301 MAYIMLCRKTSQGEHYVEAAR 321
DB 301 MAYIMLCRKTSQGEHYVEAAR 321

RESULT 2
AAQ88707
OGX14 PRELIMINARY; PRT; 321 AA.
ID OGX14
AC OGX14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE STIGMA.
GN STIGMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22867236; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehnagiri S., Simons L., Singh J., Smith V., Stinson J., Vagtes A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358341; AAQ8707.1; -.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
SQ
SEQUENCE 321 AA; 35544 MW; B2AB2E3151D39C6E CRC64;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLGLHTVDTYGRPILEVPESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
DB 1 MGILLGLLGLHTVDTYGRPILEVPESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
QY 1 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
DB 1 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
QY 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
DB 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGSTSGAPGKSLPVFAIIILISLCMVFT 300
DB 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGSTSGAPGKSLPVFAIIILISLCMVFT 300
QY 301 MAYIMLCRKTSQGEHYVEAAR 321
DB 301 MAYIMLCRKTSQGEHYVEAAR 321
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RESULT 3
OGX279 PRELIMINARY; PRT; 399 AA.
ID OGX279
AC OGX279;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 2391g protein precursor (Ig superfamily protein).
GN Name=2391g; Synonyms=2391G;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehnagiri S., Simons L., Singh J., Smith V., Stinson J., Vagtes A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358341; AAQ8707.1; -.
DR PROSITE; PSS0835; IG LIKE; 2.
SQ
SEQUENCE 321 AA; 35544 MW; B2AB2E3151D39C6E CRC64;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLGLHTVDTYGRPILEVPESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
DB 1 MGILLGLLGLHTVDTYGRPILEVPESVTGPKGVDNLPCTYDPLQGYQVLYKLVOR 60
QY 1 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
DB 1 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
QY 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
DB 181 QTNNOEPKIVATSTLLFRPAVADSGSYFCTAKGVGSQSHSDIYKPVVKDSKLLTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGSTSGAPGKSLPVFAIIILISLCMVFT 300
DB 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGSTSGAPGKSLPVFAIIILISLCMVFT 300
QY 301 MAYIMLCRKTSQGEHYVEAAR 321
DB 301 MAYIMLCRKTSQGEHYVEAAR 321
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RP SEQUENCE FROM N.A.
 RX MEDLINE=20461865; PubMed=11004523;
 RA Langnese K., Colletaux L., Kloos D.U., Fontes M., Wiesacker P.,
 RT "Cloning of Z3919, a novel gene with immunoglobulin-like domains
 located on human chromosome X.";
 RL Biochim. Biophys. Acta 1492:522-525(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadiri T.B., Toshlyuk S., Carrincci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ315502; CAB51536.1; -
 DR EMBL; BC010525; AAH10525.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 KM Signal.
 FT CHAIN 1 19 Potential.
 FT SIGNAL 20 399 2391g protein.
 SQ SEQUENCE 399 AA; 43987 MW; 735CA3BC58165035 CRC64;
 Query Match 100.0%; Score 321; DB 2; Length 399;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 MAYIMLCRKTSGQEHVEAR 321
 RESULT 4
 ID 080WA3 PRELIMINARY; PRT; 280 AA.
 AC 080WA3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein BC025105.
 GN Name=BC025105;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadiri T.B., Toshlyuk S., Carrincci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025105; AAH25105.1; -
 DR MGD; MGI:2679720; BC025105.
 DR InterPro; IPR007110; Ig-like.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 280 AA; 31467 MW; 3F099A8996CE8977 CRC64;
 Query Match 5.0%; Score 16; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1; 6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 HYTCVWTQTPDGNV 125
 RESULT 5
 ID BAC30780 PRELIMINARY; PRT; 280 AA.
 AC BAC30780;
 DT 14-APR-2004 (TREMBlrel. 27, Created)
 DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)
 DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)
 DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,
 DE clone:A530061A1 product:hypothetical Immunoglobulin and major
 DE histocompatibility complex domain/Immunoglobulin subtype containing
 DE protein, full insert sequence.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=22354683; PubMed=1246851;
 RA The PANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P.; Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P.; Shibata K.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
 RA Kono H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K.; Itoh M.; Aizawa K.; Nagata S.; Sasaki N.; Carninci P.;
 RA Kono H.; Akiyama J.; Nishi K.; Kiteunai T.; Tashiro H.; Itoh M.;
 RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;
 RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
 RA Fujiwaki S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Matshiki M.;
 RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsumura S.; Kawai J.;
 RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.;
 RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.;
 RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hiraoka T.; Hirozane T.;
 RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kaga I.; Kasukawa T.;
 RA Katoh H.; Kawai J.; Kojima Y.; Kondo S.; Kono H.; Kouda M.; Koya S.;
 RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.;
 RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohnato N.; Okazaki Y.;
 RA Saito K.; Satoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.;
 RA Sasaki D.; Shibata K.; Shinagawa A.; Shiraki T.; Sogabe Y.; Tagami M.;
 RA Tagawa A.; Takahashi F.; Takaku-Akahira S.; Takeda Y.; Tanaka T.;
 RA Tomaru A.; Toyota T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL, ARO41014; BAC30780.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 280 AA; 31467 MW; 3F099AE896CE8977 CRC64;
 QY Query Match 5.0%; Score 16; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 HYTCVWQTPDGNQV 125
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 RESULT 6
 ID Q72LB8 PRELIMINARY; PRT; 178 AA.
 AC Q72LB8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=TTCC0141;
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 NC NCB1_TaxID=262724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15064768;
 RA Henne A.; Brueggemann H.; Raasch C.; Wierzer A.; Hartsch T.;
 RA Liesegang H.; Johann A.; Lienard T.; Gohl O.; Martinez-Arias R.;
 RA Jacobi C.; Starkuviene V.; Schlenzcek S.; Dencker S.; Huber R.;
 RA Klenk H.-P.; Kramer W.; Merkl R.; Gottschalk G.; Fritze H.-J.;
 RT "The genome sequence of the extreme thermophile Thermus
 RT thermophilus."
 RL Nat. Biotechnol. 22:547-553(2004).
 DR EMBL, AEO17301; AAS80489.1; -.
 DR InterPro: IPR000252; Deda. 1.
 DR Pfam: PF00597; Deda. 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 178 AA; 19199 MW; AD34F4CC5250AB68 CRC64;
 QY Query Match 2.8%; Score 9; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 156 ILGLLLG 164
 |||||
 RESULT 7
 ID AAS80489 PRELIMINARY; PRT; 178 AA.
 AC AAS80489;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN TTC0141.
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 NC NCB1_TaxID=262724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15064768;
 RA Henne A.; Brueggemann H.; Raasch C.; Wierzer A.; Hartsch T.;
 RA Liesegang H.; Johann A.; Lienard T.; Gohl O.; Martinez-Arias R.;
 RA Jacobi C.; Starkuviene V.; Schlenzcek S.; Dencker S.; Huber R.;
 RA Klenk H.-P.; Kramer W.; Merkl R.; Gottschalk G.; Fritze H.-J.;
 RT "The genome sequence of the extreme thermophile Thermus
 RT thermophilus."
 RL Nat. Biotechnol. 22:547-553(2004).
 DR EMBL, AEO17301; AAS80489.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 178 AA; 19199 MW; AD34F4CC5250AB68 CRC64;
 QY Query Match 2.8%; Score 9; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ILGLLLLG 11
 DB 156 ILGLLLLG 164

RESULT 8
 WFD2 CANFA STANDARD; PRT; 124 AA.

AC Q28654; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE WAP four-disulfide core domain protein 2 precursor (Major epididymis-specific protein E4) (CE4) (Epididymal secretory protein E4).
 GN Name=WPD2;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epididymis;
 RX MEDLINE=95263175; PubMed=7744511;
 RA Eliebrock K., Pera I., Hartung S., Ivell R.;
 RT "Gene expression in the dog epididymis: a model for human epididymal function.";
 RL Inc. J. Androl. 17:314-323(1994).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=95263176; PubMed=7744512;
 RA Pera I., Ivell R., Kirchoff C.;
 RT "Regional variation of specific gene expression in the dog epididymis as revealed by in-situ transcript hybridization.";
 RL Int. J. Androl. 17:324-330(1994).
 CC -1- FUNCTION: Possible function in sperm maturation.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: Epididymis. Highest levels are found in the caput and proximal cauda regions. Lower levels in the distal cauda. Not detected in the efferent ducts.
 CC -1- SIMILARITY: Contains 2 WAP-type domains.
 CC
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 CC -----
 DR EMBL; S77395; AAB34264.1; -.
 DR PIR; I54768; I54768.
 DR HSSP; O46655; ICCH.
 DR InterPro; IPR008198; Prot_inh_antileu.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF00095; WAP; 2.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR ProDom; PD001224; WAP_C; 1.
 DR SMART; SM00217; WAP; 2.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
 DR KMW GlycoProtein; Repeat; Serine protease inhibitor; signal.
 FT SIGNAL 1 27
 FT CHAIN 28 124 WAP four-disulfide core domain protein 2.
 FT DOMAIN 32 74 WAP 1.
 FT DOMAIN 76 124 WAP 2.
 FT DISULFID 36 62 By similarity.
 FT DISULFID 45 66 By similarity.
 FT DISULFID 49 61 By similarity.
 FT DISULFID 55 70 By similarity.
 FT DISULFID 80 110 By similarity.
 FT DISULFID 93 114 By similarity.
 FT DISULFID 97 109 By similarity.
 FT DISULFID 103 119 By similarity.
 FT CARBOHYD 44 44 N-linked (GlcNAc...) (Potential).

SO SEQUENCE 124 AA; 12951 MW; 15AFA315RA1395AC CRC64;
 Query Match 2.5%; Score 8; DB 1; Length 124;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ILGLLLLG 11
 DB 14 ILGLLLLG 21

RESULT 9

Q7ME51 PRELIMINARY; PRT; 142 AA.

AC Q7ME51; 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein VVA0834.
 GN Name=VVA0834;
 OS Vibrio vulnificus (strain YJ016).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrrio.
 OX NCBI_Taxid=196600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14636965;
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 RT "Comparative genome analysis of *Vibrio vulnificus*, a marine pathogen.";
 RL Genome Res. 13:2577-2587(2003).
 DR EMBL; AP005347; BAC96859.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 142 AA; 16151 MW; 7A69E81D772310F5 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 308 RKTSGQEH 315
 DB 126 RKTSGQEH 133

RESULT 10

Q8PIZ1 PRELIMINARY; PRT; 217 AA.

AC Q8PIZ1; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lipoprotein.
 GN Ordered locus names=XAC2753;
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
 OX NCBI_Taxid=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Petro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., de Azevedo A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Camarvan F., Cardoso J., Chabergo J.R., Ciapina L.P., Clearelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria U.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rosel A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Trufel D., Tsal S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities";
 RL Nature 417:459-463(2002).
 DR EMBL; AE011915; AAM37599.1; -;
 DR InterPro; IPR000064; NLP_P60.
 DR Pfam; PF00877; NLP_P60; 1.
 KW Complete proteome; Lipoprotein.
 SQ SEQUENCE 217 AA; 22884 MW; 4D053E7BA92819B0 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No.25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLLGLL 11
 DB 56 ILGLLGLL 63

RESULT 11
 O8ENU3 PRELIMINARY; PRT; 222 AA.

ID O8ENU3;
 AC O8ENU3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ABC transporter permease.
 GN OrderedLocustNames=OB2383;
 OS Oceanobacillus ihayensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831;
 RX MEDLINE=2220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.,
 RT "Genome sequence of Oceanobacillus ihayensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:33927-33935(2002).
 CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
 CC Probably responsible for the translocation of the substrate across
 CC the membrane (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
 CC system permease family.
 DR EMBL; AP004601; BAC14339.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp.1; 1.
 DR PROSITE; PS50928; ABC_TMI.1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 222 AA; 24338 MW; A64DBEDBF4B8852D CRC64;

Query Match 2.5%; Score 8; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No.26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILGLL 9
 DB 36 GILGLL 43

RESULT 12
 O911J1 PRELIMINARY; PRT; 223 AA.

ID O911J1;
 AC O911J1;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=PA2284;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Hickey C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Conlter S.N., Folger K.R., Kae A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004654; AAG05672.1; -;
 DR PIR; H83359; H83359.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 223 AA; 23599 MW; 4EA632BD82AF0DB CRC64;

Query Match 2.5%; Score 8; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No.26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILGLLGLL 11
 DB 47 ILGLLGLL 54

RESULT 13
 ID MTNA METAC
 AC O8TU03; STANDARD; PRT; 240 AA.

DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Tetrahydromethanopterin S-methyltransferase subunit A (EC 2.1.1.86)
 DE (N5-methyltetrahydromethanopterin--coenzyme M methyltransferase
 DE subunit A).
 GN Name=mta; OrderedLocustNames=MA0272;
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZA / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/97.223902;
 RA Galagan J.E., Nussbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA Fitzhugh W., Galvo S., Engels R., Smirnov S., Atchop D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame J.A.,
 RA Hedderich R., Ingram-Smith C., Kuetner H.C., Kzyscki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity";
 RL Genome Res. 12:532-542(2002).
 CC -1- FUNCTION: Part of a complex that catalyzes the formation of
 CC methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
 CC methyl-tetrahydromethanopterin. This is an energy-conserving,
 CC sodium-ion translocating step (by similarity).

```

CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -1- COFACTOR: Binds 5'-hydroxybenzimidazole]-cobamide as a prosthetic
CC group (By similarity).
CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
CC mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (By similarity).
CC -1- SIMILARITY: Belongs to the mtrA family.
CC -----
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CC -----
CC EMBL: A6010686; AAM03725.1; -.
CC HAMAP: MF_01093; -.
CC InterPro: IPR005778; Met_transA.
CC Pfam: PF04208; MtrA; 1.
CC TIGRPFAMs: TIGR01111; mtrA; 1.
CC K06041; Complete proteome; Methanogenesis; Methyltransferase;
CC KM One-carbon metabolism; Transferrase; Transmembrane.
CC FT DOMAIN 1 218 Cytoplasmic (Potential).
CC TRANSMEM 219 239 Potential.
CC FT DOMAIN 240 240 Extracellular (Potential).
CC FT DOMAIN 169 176 Poly-Glu.
CC FT DOMAIN 232 238 Poly-Leu.
CC FT BINDING 85 85 5'-hydroxybenzimidazole]-cobamide
CC cofactor (By similarity).
CC SQ SEQUENCE 240 AA; 25342 MW; 86D81A2B358D2079 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILIG 11
Db 232 LIGLILIG 239

RESULT 14
MTR_A METBA STANDARD; PRT; 240 AA.
ID MTR_A METBA STANDARD; PRT; 240 AA.
AC Q9Y8K4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tetrahydromethanopterin S-methyltransferase subunit A (EC 2.1.1.86)
DE (NS-methyltetrahydromethanopterin-coenzyme M methyltransferase
DE subunit A).
GN Name:mtrA;
OS Methanosarcina barkeri.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Puaro / DSM 804;
RX MEDLINE=99268446; PubMed=10338124;
RA Hippler B., Thauer R.K.;
RT "The energy conserving methyltetrahydromethanopterin:coenzyme M
RT methyltransferase complex from methanogenic archaea: function of the
RT subunit MtrH."
RT FEBS Lett. 449:165-168(1999).
RL -1- FUNCTION: Part of a complex that catalyzes the formation of
CC methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
CC methyl-tetrahydromethanopterin. This is an energy-conserving,
CC sodium-ion translocating step (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-

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CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -1- COFACTOR: Binds 5'-hydroxybenzimidazole]-cobamide as a prosthetic
CC group (By similarity).
CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
CC mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (By similarity).
CC -1- SIMILARITY: Belongs to the mtrA family.
CC -----
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CC -----
CC EMBL: AJ132817; CAB41642.1; -.
CC HAMAP: MF_01093; -.
CC InterPro: IPR005778; Met_transA.
CC Pfam: PF04208; MtrA; 1.
CC TIGRPFAMs: TIGR01111; mtrA; 1.
CC K06041; Complete proteome; Methanogenesis; One-carbon metabolism;
CC KM Transferrase; Transmembrane.
CC FT DOMAIN 1 218 Cytoplasmic (Potential).
CC TRANSMEM 219 239 Potential.
CC FT DOMAIN 240 240 Extracellular (Potential).
CC FT DOMAIN 169 176 Poly-Glu.
CC FT DOMAIN 232 238 Poly-Leu.
CC FT BINDING 85 85 5'-hydroxybenzimidazole]-cobamide
CC cofactor (By similarity).
CC SQ SEQUENCE 240 AA; 25413 MW; A3D04EB09F6AD344 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILIG 11
Db 232 LIGLILIG 239

RESULT 15
MTR_A METBA STANDARD; PRT; 240 AA.
ID MTR_A METBA STANDARD; PRT; 240 AA.
AC O59640;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tetrahydromethanopterin S-methyltransferase subunit A (EC 2.1.1.86)
DE (NS-methyltetrahydromethanopterin-coenzyme M methyltransferase
DE subunit A).
GN Name:mtrA; OrderedLocNames=MM1543;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=98218550; PubMed=9559648;
RA Llenard T., Gottschalk G.;
RT "Cloning, sequencing and expression of the genes encoding the sodium
RT translocating NS-methyltetrahydromethanopterin:coenzyme M
RT methyltransferase of the methylotrophic archaeon Methanosarcina mazei
RT Goel."
RL FEBS Lett. 425:204-208(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Depenmeier U., Johann A., Hartach T., Merkl R., Schmitz R.A.,

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RA Martinez-Arias R., Henne A., Wierzer A., Baumeister S., Jacobl C.,
RA Bruggemann H., Lienard T., Christmann A., Bomecke M., Steckel S.,
RA Bhattacharyya A., Lytkide A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.,
RT The genome of Methanobrevibacter smithii: evidence for lateral gene
RL transfer between Bacteria and Archaea.
J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
CC -1- FUNCTION: Part of a complex that catalyzes the formation of
CC methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
CC methyl-tetrahydromethanopterin. This is an energy-conserving,
CC sodium-ion translocating step.
CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -1- COFACTOR: Binds 5'-hydroxybenzimidazole-cobamide as a prosthetic
CC group.
CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
CC mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (By similarity).
CC -1- SIMILARITY: Belongs to the mtrA family.
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CC EMBL: AF042381; AAC38334.1; -.
CC DR EMBL: AE013388; AAM31239.1; -.
CC DR HAMAP: MF_01093; -.
CC DR InterPro: IPR005778; Met_transa.
CC Pfam: PF04208; MtrA; 1.
CC TRIPDB: TRIP01111; mtrA; 1.
CC COBALT: Complete proteome; Methanogenesis; Methyltransferase;
CC One-carbon metabolism; Transferase; Transmembrane.
CC FT DOMAIN 1 218 Cytoplasmic (Potential).
CC FT TRANSMEM 219 239 Potential.
CC FT DOMAIN 240 240 Extracellular (Potential).
CC FT DOMAIN 169 176 Poly-Glu.
CC FT BINDING 85 85 5'-hydroxybenzimidazole-cobamide
CC cofactor (By similarity).
CC FT CONFLICT 16 16 G -> R (in Ref. 1).
CC FT CONFLICT 71 71 N -> D (in Ref. 1).
CC FT CONFLICT 127 127 E -> G (in Ref. 1).
CC FT CONFLICT 161 161 D -> E (in Ref. 1).
CC FT SEQUENCE 240 AA; 25366 MW; 44C086DD3561E526 CRC64;
SQ
Query Match 2.5%; Score 8; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LIGLILIG 11
DB 232 LIGLILIG 239
RESULT 16
Q6XP4 PRELIMINARY; PRT; 249 AA.
AC Q6XP4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS Transmembrane receptor PcgammarIII-X.
DS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RA Teusner J.T., Belford D.A., Powell B.C.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY219230; AAP44530.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PR00047; Ig_2.
DR SMART: SM00409; Ig_2.
DR SMART: SM00408; Ig_c2; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
KW Receptor; Transmembrane.
SQ SEQUENCE 249 AA; 28168 MW; C58B6B2B97595D21 CRC64;
Query Match 2.5%; Score 8; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 204 ADSGSYFC 211
DB 164 ADSGSYFC 171
RESULT 17
AAP44530 PRELIMINARY; PRT; 249 AA.
AC AAP44530;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DS Transmembrane receptor PcgammarIII-X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Teusner J.T., Belford D.A., Powell B.C.,
RL Identification of a novel rat receptor homologous to human
RL PcgammarIII-A.
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY219230; AAP44530.1; -.
KW Receptor; Transmembrane.
SQ SEQUENCE 249 AA; 28168 MW; C58B6B2B97595D21 CRC64;
Query Match 2.5%; Score 8; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 204 ADSGSYFC 211
DB 164 ADSGSYFC 171
RESULT 18
Q46648 PRELIMINARY; PRT; 265 AA.
AC Q46648;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DS Name-hrcT;
OS Brwnia amylovora.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Brwnia.
OX NCBI_TaxID=552;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=321;
RX MEDLINE=96198177; PubMed=8626302;
RA Bogdanove A.J., Wei Z.M., Zhao L., Beer S.V.,

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RT "Bawinia amylovora secretes harpin via a type III pathway and contains
a homolog of yopN of Yersinia spp.";
RL J. Bacteriol. 178:1720-1730(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: L25828; AAB06007.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0006605; P:protein targeting; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR006304; SPAR_Yact.
DR InterPro: IPR002010; TYPE3IMPRPROT.
DR Pfam: PF01311; Bac_export_1; 1.
DR PRINTS: PR00953; TYPE3IMPRPROT.
DR TIGRFAMs: TIGR01401; flir_like_III; 1.
KM Tmembrane.
SQ SEQUENCE 265 AA; 28988 MW; C3B5FD87BCC23D2 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILGLLL 9
DB 83 GILGLLL 90

RESULT 19
Q95KP8 PRELIMINARY; PRT; 269 AA.
AC Q95KP8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sialic acid-binding lectin Siglec-L1 (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_Taxid=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL: AY029757; AAKS0564.1; -.
DR HSSP: Q9Y286; 107S.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_2.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Lectin.
FT NON TER 269
SQ SEQUENCE 269 AA; 30649 MW; D2127734EBC3C7CA CRC64;

Query Match 2.5%; Score 8; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESVT 30
DB 153 LEVPESVT 160

RESULT 20
Q95KP9 PRELIMINARY; PRT; 269 AA.
AC Q95KP9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sialic acid-binding lectin Siglec-L1 (Fragment).
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_Taxid=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL: AY029754; AAKS0563.1; -.
DR HSSP: Q9Y286; 107S.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_2.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Lectin.
FT NON TER 269
SQ SEQUENCE 269 AA; 30436 MW; 96E49EAF779D6E50 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESVT 30
DB 153 LEVPESVT 160

RESULT 21
Q95KQ0 PRELIMINARY; PRT; 271 AA.
AC Q95KQ0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sialic acid-binding lectin Siglec-L1 (Fragment).
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_Taxid=9597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL: AY029753; AAKS0562.1; -.
DR HSSP: Q9Y286; 107S.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_2.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Lectin.
FT NON TER 271
SQ SEQUENCE 271 AA; 30613 MW; F63B6018C1C7B934 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESVT 30
DB 153 LEVPESVT 160

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Db 155 LEVESVT 162

RESULT 22

Q6SFH9 PRELIMINARY; PRT; 292 AA.
 ID Q6SFH9
 AC Q6SFH9;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN ORFNames=EBAC000-36A07.83;
 OS uncultured bacterium 580.
 OC Bacteria; environmental samples.
 NCBI_TaxID=257400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA DeLong E.F.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Heidelberg J.F., Bisen J.A., Nelson W.C., DeLong E.F.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY458647; AAR38238.1; -.
 DR InterPro; IPR000620; DUF6.
 DR Pfam; PF00892; DUF6; 2.
 DR SEQUENCE 292 AA; 32975 MW; E3A21B8F65BB9D14 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 292;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILGLLL 10
 Db 277 ILGLLL 284

RESULT 23
 AAR38238 PRELIMINARY; PRT; 292 AA.
 ID AAR38238
 AC AAR38238;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN EBAC000-36A07.83.
 OS uncultured bacterium 580.
 OC Bacteria; environmental samples.
 NCBI_TaxID=257400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA DeLong E.F.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Heidelberg J.F., Bisen J.A., Nelson W.C., DeLong E.F.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY458647; AAR38238.1; -.
 DR SEQUENCE 292 AA; 32975 MW; E3A21B8F65BB9D14 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 292;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILGLLL 10
 Db 277 ILGLLL 284

RESULT 24

ID Q702H2 PRELIMINARY; PRT; 346 AA.
 AC Q702H2;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Organic anion transporter 2 (Fragment).
 GN Name=cat2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Geyer J., Petzinger E.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AJ627253; CAF28454.1; -.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub transporter.
 DR Pfam; PF00083; Sugar tr_1.
 DR PROSITE; PS50850; MFS; 1.
 KW Transmembrane.
 FT NON TER 1
 FT NON TER 346
 FT SEQUENCE 346 AA; 38394 MW; 96508FAD632FE096 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 ISLCMVV 298
 Db 231 ISLCMVV 238

RESULT 25
 CAF28454 PRELIMINARY; PRT; 346 AA.
 ID CAF28454
 AC CAF28454;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Organic anion transporter 2 (Fragment).
 GN CAT2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Geyer J., Petzinger E.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ627253; CAF28454.1; -.
 FT NON TER 1
 FT NON TER 346
 FT SEQUENCE 346 AA; 38394 MW; 96508FAD632FE096 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 ISLCMVV 298
 Db 231 ISLCMVV 238

RESULT 26

Q9GJEB


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ID 09GJ33 PRELIMINARY; PRT; 350 AA.
AC 09GJ33;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE MHC class I antigen.
GN Name:Mamc-I;
OS Mamota monax (woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuriidae; Scuriinae;
OC Mamoca.
CX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang D.-L., Zhou J.-H., Lu M., Gross-Wild H., Roggendorf M.;
RT "There are at least two loci in woodchuck MHC class I gene.";
RL EMBL/AF201912; AAC3957.1; -.
DR HSSP; Q29961; IHS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-1ike.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CL-sec; 1.
DR Pfam; PF00129; MHC_1; 1.
DR PRINTS; PRO1638; MHCCLASSI.
DR PRODOM; PD000050; MHC_1; 1.
DR SMART; SMO0407; IGL; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Transmembrane.
SQ SEQUENCE 350 AA; 40772 MW; 629E9B7BDF8472F1 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILGILL 9
DB 307 GILGILL 314

RESULT 27
Q6TV6 PRELIMINARY; PRT; 366 AA.
AC 06TV6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE 57L.
OS Yaba monkey tumor virus (YMTV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
CX NCBI_TaxID=38804;
RN [1]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RT "A secreted high-affinity inhibitor of human TNF from Tanapox virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4831-4836(2003).
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=95248279; PubMed=7730796;
RA Amano H., Ueda Y., Miyamura T.;
RT "Identification and characterization of the thymidine kinase gene of
RT Yaba virus.";
RL J. Gen. Virol. 76:1109-1115(1995).
[3]
RP SEQUENCE FROM N.A.
RX PubMed=14645589;

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RA Brunetti C.R., Amano H., Ueda Y., Qin J., Miyamura T., Suzuki T.,
RA Li X., Barrett J.W., McFadden G.;
RT "Complete genomic sequence and comparative analysis of the tumorigenic
RT poxvirus Yaba monkey tumor virus.";
RL J. Virol. 77:13335-13347(2003).
[4]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR008787; Pox_G7.
DR Pfam; PF05503; Pox_G7; 1.
SQ SEQUENCE 366 AA; 41961 MW; 3B8F0CDE2053A82F CRC64;

Query Match 2.5%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 VATLSTLL 197
DB 116 VATLSTLL 123

RESULT 28
AA07413 PRELIMINARY; PRT; 366 AA.
ID AA07413;
AC AA07413;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE 57L.
OS Yaba monkey tumor virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
CX NCBI_TaxID=38804;
RN [1]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Amano H., Ueda Y., Qin J., Miyamura T., Suzuki T.,
RA Li X., Barrett J.W., McFadden G.;
RT "Complete Genomic Sequence and Comparative Analysis of the Tumorigenic
RT poxvirus Yaba Monkey Tumor Virus.";
RL J. Virol. 77:13335-13347(2003).
[2]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RT "A secreted high-affinity inhibitor of human TNF from Tanapox virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4831-4836(2003).
[4]
RP SEQUENCE FROM N.A.
RA Brunetti C.R., Paulose-Murphy M., Singh R., Qin J., Barrett J.W.,
RA Tardivel A., Schneider P., Essani K., McFadden G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY386371; AA07413.1; -.
SQ SEQUENCE 366 AA; 41961 MW; 3B8F0CDE2053A82F CRC64;

Query Match 2.5%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 VATLSTLL 197
DB 116 VATLSTLL 123

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RESULT 29
030187 PRELIMINARY; PRT; 412 AA.
AC 030187;
DT 01-JAN-1998 (TEMBurel. 05, Created)
DT 01-JUN-1998 (TEMBurel. 05, Last sequence update)
DT 01-JUN-2003 (TEMBurel. 25, Last annotation update)
DE Hypothetical protein AF0049.
OS OrderedLocNames=AF0049;
OC Archaeoglobus fulgidus.
OC Archaeoglobaceae; Archaeoglobales;
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobus;
OX NCBI_TaxID=2234;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickley E.K., Peterson J.D.,
RA Reichmann D.L., Kerevashvili U., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkeess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodex A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Utecherback T.R., Cotton M.D., Spriggs T., Artlich P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Moese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AE001103; AAB91183.1; -.
DR PIR; A69256; A69256.
DR TIGR; AF0049; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 412 AA; 45909 MW; 6A23FBF73640E310 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 YIGETSAG 277
|||||
142 YIGETSAG 149

DB
RESULT 30
PSL2 HUMAN STANDARD; PRT; 520 AA.
ID PSL2_HUMAN
AC OBT8; OBT8; OBT8; OBT8; OBT8; OBT8; OBT8; OBT8; OBT8; OBT8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Signal peptide peptidase-like 2A (EC 3.4.99.-) (SPP-1 like 2A protein)
DE (SPP1a peptidase) (intramembrane protease 3) (IMP3) (Presentin-1 like
DE protein 2).
GN Name=SPP1a; Synonyms=PSL2;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC Irmeler M., Tomiuk S., Korner M.R., Hofmann K., Conradt M.;
RT "Characterization of a new protein family with homology to
RT presentin-1."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22135308; PubMed=12139484;
RA Gligorenko A.P., Mollata Y.K., Korovaitseva G.I., Rogaev E.I.;

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RT "Novel class of polycyclic proteins with domains associated with
RT putative protease activity."
RL Biokhimiia 67:826-834(2002).
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Oca T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto Y., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Pancereas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedln T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton B., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield J.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP SEQUENCE OF 91-520 FROM N.A.
RC TISSUE=Testicocarcinoma;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Iehidashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,
RA Iehida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Houta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyasu S., Komai F., Hara R., Takuchi K., Arita M.,
RA Imose N., Mutsaers K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakiue H.,
RA Hishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujitani T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Omori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunaga K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi K., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
RN
RP SEQUENCE OF 91-520 FROM N.A.
RC TISSUE=Cervical carcinoma;

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RX MEDLINE=22072745; PubMed=12077416; DOI=10.1126/science.1070925;
RA Wehlofen A., Bims K., Lemberg M.K., Ashman K., Martoglio B.;
RT "Identification of signal peptide peptidase, a presenilin-type
RL separate protease."
RL Science 296:2215-2218 (2002).
CC -1- FUNCTION: May act as intramembrane protease.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the presenilin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ345028; CAC8789.1; -
DR EMBL; AY169314; AA012539.1; -
DR EMBL; AK075454; BA011630.1; -
DR EMBL; BC025740; AA025740.1; -
DR EMBL; AK027446; BAB5117.1; ALT_INIT.
DR EMBL; AJ420896; CAD1313.1; ALT_INIT.
DR MEROPS; A22.007; -
DR MIM; 608238; -
DR InterPro; IPR003137; PA.
DR InterPro; IPR006639; Peptidase_A22.
DR InterPro; IPR007369; Peptidase_A22B.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04258; Peptidase_A22B; 1.
DR SMART; SM00730; PSN; 1.
DR Hydrobase; Protease; Transmembrane.
KW DOMAIN 1 172 Cytoplasmic (Potential).
FT TRANSMEM 173 193 Potential.
FT TRANSMEM 221 241 Potential.
FT TRANSMEM 248 268 Potential.
FT TRANSMEM 286 306 Potential.
FT TRANSMEM 312 332 Potential.
FT TRANSMEM 341 361 Potential.
FT TRANSMEM 400 420 Potential.
FT TRANSMEM 438 458 Potential.
FT TRANSMEM 461 481 Potential.
FT DOMAIN 55 152 PA.
FT CONFLICT 126 126 N -> D (in Ref. 5).
FT CONFLICT 271 271 I -> T (in Ref. 3).
FT CONFLICT 406 406 S -> L (in Ref. 3).
FT CONFLICT 446 446 I -> F (in Ref. 3).
FT CONFLICT 511 511 V -> E (in Ref. 5).
SQ SEQUENCE 520 AA; 58143 MW; A7A933A6504507DC CRC64;

Query Match 2.5%; Score 8; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILGLLL 10
Db 342 ILGLLL 349

RESULT 31
ID OTOIRO PRELIMINARY; PRT; 537 AA.
AC OTOIRO;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE AGCP3417 (Fragment).
DE Name=agCG54408; ORFname=ENSANGC00000012635;
OS Anopheles gambiae str. PBST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA00100807; EA04152.1; -
DR GO; GO:0016758; P:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glycosyl_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 537 AA; 59693 MW; 5B495D82947DCD1 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ILGLLL 11
Db 21 ILGLLL 28

RESULT 32
ID O6BSF5 PRELIMINARY; PRT; 590 AA.
AC O6BSF5;
DT 01-OCT-2004 (Tremblrel. 28, Created)
DT 01-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Similar to CA1037[CamMS1 Candida albicans CamMS1.
DE ORFname=DEHA0D101539;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barde V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrame A., Boyer J., Cartolico L., Confariolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolaki M., Ozas S., Ozler-Kalogeropoulou O.,
RA Pellenz S., Porter S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Jouvet M., Westhof E., Wirth B.,
RA Zentou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382136; CAC87017.1; -
SQ SEQUENCE 590 AA; 67544 MW; B06BED6770A98228 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 590;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 QTNQBP 188

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FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
FT VARSPIC 4 141 LILLLPILGKRGKAGKOKYLLTMOSSVTVRELCVSYLC
FT SPSYFQNGRTASDSDVHWGTPRAGDHSNIPATNNPARY
FT QETRDPRFHLGSDPQNDCTSLIDTRESNAGTVPCVERG
FT NMKNVXYKXDLSVVV -> PLTMANBERSDGSMADPRFS
FT (in isoform short).
FT /FTID=VSP_002566.
FT P -> T (in dbSNP:2034691).
FT /FTID=VAR_014259.
FT R -> W (in Ref. 3).
SQ SEQUENCE 595 AA; 64984 MW; D05662176274C5C3 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 595;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESTV 30
Db 153 LEVPESTV 160

RESULT 34
SILL_PANTR STANDARD; PRT; 597 AA.
AC 095LHO;
DT 28-FEB-2003 (Ref. 41, Created)
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 01-OCT-2004 (Ref. 45, Last annotation update)
DE Sialic acid binding Ig-1 like lectin-like 1 precursor (Siglec-1)
DE molecule 1) (Siglec-1).
GN Name=SIGLECI;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OC NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
RA Aigata T., Varki N.M., Varki A.;
RT A second uniquely human mutation affecting sialic acid biology.;
RL J. Biol. Chem. 276:40282-40287(2001).
CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC dependent binding to cells. The sialic acid recognition site may
CC be masked by cis interactions with sialic acids on the same cell
CC surface.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
CC motif is involved in modulation of cellular responses. The
CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC containing phosphatases.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AF293372; AAL09302.1; -
DR HSSP; Q9Y286; 107S.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KM Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
Signal; Transmembrane.

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FT SIGNAL 1 20 Potential.
FT CHAIN 21 597 Sialic acid binding Ig-1 like lectin-like
FT 1.
FT DOMAIN 21 483 Extracellular (Potential).
FT TRANSMEM 484 504 Potential.
FT DOMAIN 505 597 Cytoplasmic (Potential).
FT DOMAIN 21 144 Ig-1 like V-type 1.
FT DOMAIN 145 271 Ig-1 like V-type 2.
FT DOMAIN 277 360 Ig-1 like C2-type 1.
FT DOMAIN 367 460 Ig-1 like C2-type 2.
FT SITE 565 570 ITIM motif.
FT SITE 588 593 SLAM-LIKE MOTIF.
FT DISULFID 46 106 By similarity.
FT DISULFID 168 301 By similarity.
FT DISULFID 173 233 By similarity.
FT DISULFID 295 344 By similarity.
FT DISULFID 403 448 By similarity.
FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 362 362 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 387 387 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 597 AA; 65075 MW; 74C13CFA9CDB5B85 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 597;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LEVPESTV 30
Db 155 LEVPESTV 162

RESULT 35
O6IBL2
ID O6IBL2 PRELIMINARY; PRT; 612 AA.
AC O6IBL2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE OS-9 protein.
GN Name=OS-9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schlick W., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CRA56791; CAG33072.1; -
DR InterPro; IPR009011; Man6php_recept.
SQ SEQUENCE 612 AA; 69232 MW; FC6854FFB1B26ED CRC64;

Query Match 2.5%; Score 8; DB 2; Length 612;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGILLIG 11
Db 10 LIGILLIG 17

RESULT 36
Q9BW99 PRELIMINARY; PRT; 612 AA.
ID Q9BW99;
AC Q9BW99; Q8I258;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE OS-9 protein.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toohily S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC000532; AA00532.1; -.
DR EMBL; BC007254; AA07254.1; -.
DR EMBL; BC023513; AA023513.2; -.
DR InterPro; IPR009011; ManGnp_Recept.
SQ SEQUENCE 612 AA; 69246 MW; 1FD06F7B23101015 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGILLIG 11
DB 10 LIGILLIG 17

RESULT 37
CAG33072 PRELIMINARY; PRT; 612 AA.
AC CAG33072;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE OS-9 protein.
GN OS-9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.

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RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456791; CAG33072.1; -.
SQ SEQUENCE 612 AA; 69232 MW; FC6854FEF11B26BD CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGILLIG 11
DB 10 LIGILLIG 17

RESULT 38
C6JH13 PRELIMINARY; PRT; 655 AA.
AC C6JH13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thrombospondin-related anonymous protein.
GN Name=trap;
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Israel C61411;
RX PubMed=15138064;
RA Gaffar F.R., Yatsuda A.P., Franssen F.F., Vries Ed B.;
RT "A Babesia bovis merozoite protein with a domain architecture highly
RT similar to the thrombospondin-related anonymous protein (TRAP) present
RT in Plasmodium sporozoites.";
RL Mol. Biochem. Parasitol. 136:25-34(2004).
DR EMBL; AY486102; AAS58046.1; -.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VMA_1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VMA_1.
DR PROSITE; PSS0234; VWFPA_1.
SQ SEQUENCE 655 AA; 71322 MW; 4FF6306B480BD3F5 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGILLIG 11
DB 595 LIGILLIG 602

RESULT 39
AAS58046 PRELIMINARY; PRT; 655 AA.
AC AAS58046;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Thrombospondin-related anonymous protein.
GN TRAP.
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Israel C61411;
RX PubMed=15138064;
RA Gaffar F.R., Yatsuda A.P., Franssen F.F., Vries Ed B.;
RT "A Babesia bovis merozoite protein with a domain architecture highly
RT similar to the thrombospondin-related anonymous protein (TRAP) present

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DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00490; HELIC_C; 1.
 DR TIGRPFAM; TIGR01587; Cae3_core; 1.
 KW Complete proteome; Helicase.
 SQ SEQUENCE 750 AA; 84879 MW; B075B49FA0EDBCB7 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 KSLPVPFAL 287
 |||||
 Db 555 KSLPVPFAL 562

RESULT 42
 AAS69549 PRELIMINARY; PRT; 750 AA.
 ID AAS69549;
 AC AAS69549;
 DT 24-MAR-2004 (TrEMBLrel. 27, Created)
 DT 24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE ATP-dependent RNA helicase.
 GN IIC10938.
 OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni).
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 NC NCBI_TaxID=44275;
 RN (1)
 SEQUENCE FROM N.A.
 RC STRAIN=Flacruiz L1-130;
 RX PubMed=15028702;
 RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorcello C.B.,
 Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeel R.A.,
 Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carter H.,
 Coutinho L.B., Degraeve W.M., Delagostin O.A., El-Dorri H.,
 RA Perro E.S., Ferro M.I.T., Furlan L.R., Gambellini M., Gagliotti E.A.,
 RA Goes-Neto A., Goldman G.H., Goldman M.S., Harakava R.,
 RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
 RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
 RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
 RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
 RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
 RT "Comparative genomics of two Leptospira interrogans serovars reveals
 novel insights into physiology and pathogenesis.";
 RL J. Bacteriol. 186:2164-2172(2004).
 DR EMBL; AB017290; AAS69549.1; -.
 KW Helicase.
 SQ SEQUENCE 750 AA; 84879 MW; B075B49FA0EDBCB7 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 KSLPVPFAL 287
 |||||
 Db 555 KSLPVPFAL 562

RESULT 43
 Q8F1E6 PRELIMINARY; PRT; 752 AA.
 ID Q8F1E6;
 AC Q8F1E6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ATP-dependent RNA helicase, putative.
 GN Leptospira interrogans.
 OS Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OC NCBI_TaxID=173;
 RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RX MEDLINE=22598143; PubMed=12712204;
 RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
 RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
 RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
 RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
 RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia O.-C., Guo X.-K., Danchin A.,
 RA Saint-Giron I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
 RA Xu J.-G., Zhao G.-P.;
 RT "Unique physiological and pathogenic features of Leptospira
 RT Interrogans revealed by whole-genome sequencing.";
 RL Nature 423:888-893(2003).
 DR EMBL; AE011481; AAN50388.1; -.
 DR GO; GO:0005524; P.ATP binding; IEA.
 DR GO; GO:0008026; P.ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; P.hydrolase activity; IEA.
 DR GO; GO:0003676; P.nucleic acid binding; IEA.
 DR InterPro; IPR006474; Cae3_core.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC_C; 1.
 DR TIGRPFAM; TIGR01587; Cae3_core; 1.
 KW ATP-binding; Complete proteome; Helicase; Hydrolase.
 SQ SEQUENCE 752 AA; 85093 MW; 2B71E8F572385C0B CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 KSLPVPFAL 287
 |||||
 Db 555 KSLPVPFAL 562

RESULT 44
 Q86AH2 PRELIMINARY; PRT; 937 AA.
 ID Q86AH2;
 AC Q86AH2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similar to Dictyostelium discoideum (Slime mold).
 DB Kda protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
 NC NCBI_TaxID=44689;
 RN (1)
 SEQUENCE FROM N.A.
 RP STRAIN=AX4;
 RC MEDLINE=22092622; PubMed=12097910;
 RX Gloeckner G., Eichinger L., Szafranski K., Pachbat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guiso R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzner M., Rosenthal A., Nogel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 RL Nature 418:79-85(2002).
 RN (2)
 SEQUENCE FROM N.A.
 RP STRAIN=AX4;
 RC Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC115599; AAO51504.1; -.
 DR InterPro; IPR008615; FNIP.
 DR Pfam; PF05725; FNIP; 4.
 KW Hypothetical protein.
 SQ SEQUENCE 937 AA; 105880 MW; BEC2F6A936489778 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 99;
 2.5%; Score 8; DB 2; Length 937;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 NOVVRDKI 130
 |||||
 Db 115 NOVVRDKI 122

RESULT 45

CHRD_MOUSE STANDARD; PRT; 948 AA.

AC Q920E2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chordin precursor.
 GN Name=Chrd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RC STRAIN=B6SJL/F1;
 RA Lu B., Bachiller D., Agius E., Piccolo S., De Robertis E.M.;
 RT "BMP-binding domains in the chordin secreted protein.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.
 [2]
 RA MEDLINE=99000848; PubMed=9782094;
 RA Pappano W.N., Scott I.C., Clark T.G., Eddy R.L., Shows T.B.,
 RA Greenspan D.S.;
 RT "Coding sequence and expression patterns of mouse chordin and mapping
 of the cognate mouse chrd and human CHRD genes.";
 RL Genomics 52:236-239(1998).
 CC -1- FUNCTION: Dorsalizing factor. Key developmental protein that
 dorsalizes early vertebrate embryonic tissues by binding to
 ventralizing TGF-beta family bone morphogenetic proteins (BMPs)
 and sequestering them in latent complexes.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- DEVELOPMENTAL STAGE: Detected at high levels of a in 7 dpc mouse
 embryos; its level decrease at later developmental stages and in
 adult tissues.
 CC -1- SIMILARITY: Belongs to the chordin family.
 CC -1- SIMILARITY: Contains 4 CHRD domains.
 CC -1- SIMILARITY: Contains 4 WWC domains.
 CC -1- SIMILARITY: Contains 4 WWC domains.
 CC -----
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 CC -----
 DR EMBL; AF096276; AA019895.1; -
 DR EMBL; AF096501; AAC68867.1; -
 DR MGD; MGI:1313268; Chrd.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0009953; P:dorsal/ventral pattern formation; IMP.
 DR GO; GO:0010003; P:gastrulation (sensu Mammalia); IMP.
 DR GO; GO:0001501; P:skeletal development; IMP.
 DR InterPro; IPR010895; CHRD.
 DR InterPro; IPR006559; SOG.
 DR InterPro; IPR001007; WWC_C.
 DR Pfam; PF07452; CHRD; 4.
 DR Pfam; PF00093; WWC; 4.
 DR SMART; SM00566; SOG; 3.
 DR SMART; SM00214; WWC; 4.
 DR PROSITE; PS50933; CHRD; 4.
 DR PROSITE; PS501208; WWC_1; 2.
 DR PROSITE; PS50184; WWC_2; 2.
 KW Developmental protein; Glycoprotein; Repeat; signal.
 FT SIGNAL 1 26 Potential.

FT CHAIN 27 948 Chordin.
 FT DOMAIN 49 126 WWC 1.
 FT DOMAIN 168 277 CHRD 1.
 FT DOMAIN 279 398 CHRD 2.
 FT DOMAIN 399 520 CHRD 3.
 FT DOMAIN 526 646 CHRD 4.
 FT DOMAIN 699 759 WWC 2.
 FT DOMAIN 779 845 WWC 3.
 FT DOMAIN 867 927 WWC 4.
 FT CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 430 430 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 877 877 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 948 AA; 101512 MW; 853117C5D1739E63 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 948;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLLLG 11
 |||||
 Db 13 LIGLLLG 20

RESULT 46

OGUW83 PRELIMINARY; PRT; 954 AA.

ID OGUW83;
 AC OGUW83;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Chordin.
 GN ORFNames=UNQ217;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309;
 RX Clark H.F., Gurney A.L., Abaya E., Baker K., Balwin D., Brush J.,
 RA Chon J., Chow B., Chui C., Crowley C., Gu Q., Hess P.E., Heide S.,
 RA Baton D., Foster J., Grimlidi C., Gu Q., Hess P.E., Heide S.,
 RA Huang L., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vanden R., Watanabe C., Wietand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RT Genome Res. 13:2265-2270(2003).
 RL EMBL; AY358926; AA089285.1; -
 DR EMBL; AY358926; AA089285.1; -
 DR InterPro; IPR010895; CHRD.
 DR InterPro; IPR009041; BMP_SGCT.
 DR InterPro; IPR006559; SOG.
 DR InterPro; IPR001007; WWC_C.
 DR Pfam; PF07452; CHRD; 4.
 DR Pfam; PF00093; WWC; 4.
 DR SMART; SM00566; SOG; 3.
 DR SMART; SM00214; WWC; 4.
 DR PROSITE; PS50933; CHRD; 4.
 DR PROSITE; PS01208; WWC_1; 2.
 DR PROSITE; PS50184; WWC_2; 2.
 SQ SEQUENCE 954 AA; 101959 MW; 853117C5D1739E63 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 954;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLLLG 11
 |||||
 Db 13 LIGLLLG 20

```

RESULT 47
AA089285 PRELIMINARY; PRT; 954 AA.
ID AA089285;
AC AA089285;
DT 02-MAR-2004 (TEMBREL. 27, Created)
DT 02-MAR-2004 (TEMBREL. 27, Last sequence update)
DT 02-MAR-2004 (TEMBREL. 27, Last annotation update)
DE Chordin.
GN UNQ217.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu O., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark W., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagitt S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY58926; AA089285.1; -;
SQ SEQUENCE 954 AA; 101959 MW; 853317C5D1739E63 CRC64;

Query Match 2.5%; Score 8; DB 2; Length 954;
Best Local Similarity 100.0%; Pred.No.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLGLLGL 11
Db 13 LGLGLLGL 20

RESULT 48
CHRD_HUMAN STANDARD; PRT; 955 AA.
ID CHRD_HUMAN
AC Q9H2X0; Q9S254; Q9H2D3; Q9H2W8; Q9H2W9; Q9P0Z2; Q9P0Z3; Q9P0Z4;
AC Q9P0Z5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chordin precursor.
GN Name=CHRD;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RX MEDLINE=21366001; PubMed=11472837;
RA Millet C., Lemaitre P., Orsetti B., Guglielmi P., Francois V.;
RT "The human chordin gene encodes several differentially expressed
RT spliced variants with distinct BMP opposing activities.";
RL Mech. Dev. 106:85-96(2001).

[2]
RP SEQUENCE OF 115-955 FROM N.A. (ISOFORM 5).
RX MEDLINE=99000848; PubMed=782094;
RA Pappano W.N., Scott I.C., Clark T.G., Eddy R.L., Shows T.B.,
RA Greenspan D.S.;
RT "Coding sequence and expression patterns of mouse chordin and mapping
RT of the cognate mouse chrd and human CHRD genes.";
RL Genomics 52:236-239(1998).
[3]

```

```

RP SEQUENCE OF 51-125; 705-762; 784-850 AND 872-932 FROM N.A.
RX MEDLINE=20115435; PubMed=10648240;
RA Iarrin J., Bachiller D., Lu B., Agius E., Piccolo S.,
RA de Robertis E.M.;
RT "BMP-binding modules in chordin: a model for signalling regulation in
RT the extracellular space.";
RL Development 127:821-830(2000).
RN [4]
RP SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.B.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -1- FUNCTION: Dorsalizing factor. Key developmental protein that
CC dorsalizes early vertebrate embryonic tissues by binding to
CC and sequestering them in latent complexes (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC isoforms;
CC Name=1;
CC IsoId=Q9H2X0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H2X0-2; Sequence=VSP_001069, VSP_001070;
CC Name=3;
CC IsoId=Q9H2X0-3; Sequence=VSP_001071, VSP_001072;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=4;
CC IsoId=Q9H2X0-4; Sequence=VSP_001073, VSP_001074;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=5;
CC IsoId=Q9H2X0-5; Sequence=VSP_001075;
CC -1- TISSUE SPECIFICITY: Expressed at the highest level in liver.
CC -1- SIMILARITY: Belongs to the chordin family.
CC -1- SIMILARITY: Contains 4 CHRD domains.
CC -1- SIMILARITY: Contains 4 WMFC domains.
CC -----
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CC -----
CC EMBL; AF209928; AAC35767.1; -;
CC EMBL; AF209929; AAC35768.1; -;
CC DR EMBL; AF209930; AAC35769.1; -;
CC DR EMBL; AF076612; AAC69835.1; -;
CC DR EMBL; AF283325; AAC69835.1; -;
CC DR EMBL; AF136632; AAF70236.1; -;
CC DR EMBL; AF136633; AAF70237.1; -;
CC DR EMBL; AF136634; AAF70238.1; -;
CC DR EMBL; AF136635; AAF70239.1; -;
CC DR Genew; HGNC:1949; CHRD.
CC MIM; 603475; -;
CC GO; GO:0001501; P:skeletal development; TAS.
CC DR InterPro; IPR010895; CHRD.
CC DR InterPro; IPR001007; WMFC.
CC DR Pfam; PF07452; CHRD; 4.
CC DR Pfam; PF00093; WMFC; 4.
CC DR PROSITE; PS50933; CHRD; 4.
CC DR PROSITE; PS01208; WMFC_1; 2.
CC DR PROSITE; PS01208; WMFC_2; 2.
CC KW Alternative splicing; Developmental protein; Glycoprotein; Repeat;
CC Signal.
CC FT SIGNAL 1 26 Potential.
CC FT CHAIN 27 955 Chordin.
CC FT DOMAIN 49 126 WMFC 1.

```

RESULT	49
ID	Q86G86
AC	Q86G86
DT	01-JUN-2003 (TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Integrin alpha 3
OS	Pseudoplusia includens (Soybean looper).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea
OC	Noctuidae; Plusiinae; Pseudoplusia.
OX	NCBI_TaxID=76492;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22855736; PubMed=12974949;
RA	Lavigne M.D., Strand M.R.;
RT	"Haemocytes from Pseudoplusia includens express multiple alpha and beta integrin subunits."
CC	Insect Mol. Biol. 12:441-452(2003).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC	-1- SIMILARITY: Belongs to the integrin alpha chain family.
CC	EMBL; AY375877; AAO5805.1; ..
DR	GO; GO:0008305; C:integrin complex; IEA.
DR	GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR	GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR	InterPro; IPRO00413; Integrin_alpha.
DR	Pfam; PF01839; FG-GAP; 2.
DR	PRINTS; PRO0185; INTEGRIN.
DR	SMART; SM00191; Int_alpha; 6.
DR	PROSITE; PS00242; INTEGRIN_ALPHA; UNKOWN_1.
DR	Cell adhesion; Integrin; Transmembrane.

RT "Tissue-specific expression, induction, and inhibition through
 RT metabolic intermediate-complex formation of guinea pig cytochrome P450
 RT Arch. Biochem. Biophys. 239:248-254(1992).
 RT Arch. Biochem. Biophys. 239:248-254(1992).
 SQ SEQUENCE 31 AA; 3396 MW; F05B04E2557458AC CRC64;

Query Match 2.2%; Score 7; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLL 10
 Db 12 LGGLLLL 18

RESULT 52

Q9QVU4 PRELIMINARY; PRT; 33 AA.

AC Q9QVU4; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE Cytochrome P450GP-1 (Fragment).

OS Cavia (guinea pigs).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae.

OX NCBI_TaxID=10140;

RN [1]

RP SEQUENCE

RX MEDLINE=1378369; PubMed=1897986;

RA Oguri K., Kaneko H., Tanimoto Y., Yamada H., Yoshimura H.;

RT "A constitutive form of guinea pig liver cytochrome P450 closely

RT related to phenobarbital inducible P450b(e).";

DR Arch. Biochem. Biophys. 287:105-111(1991).

FT PIR; S15135; A36154.

FT NON_TER 33

SQ SEQUENCE 33 AA; 3550 MW; 1202B05B04E25574 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLL 10
 Db 12 LGGLLLL 18

RESULT 53

Q9QVU1 PRELIMINARY; PRT; 41 AA.

AC Q9QVU1; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE Cytochrome P450GP-1 (Fragment).

OS Cavia (guinea pigs).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae.

OX NCBI_TaxID=10140;

RN [1]

RP SEQUENCE

RX MEDLINE=96118203; PubMed=8553686;

RA Chung W.G., Miranda C.L., Buhler D.R.;

RT "A cytochrome P450GP form is the major bioactivation enzyme for the

RT pyrolytic alkaloid senecionine in guinea pig.;"

RT xenobiotica 25:929-939(1995).

SQ SEQUENCE 41 AA; 4409 MW; C414BCAF317671C0 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 41;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLL 10

Db 12 LGGLLLL 18

RESULT 54

Q70BW1 PRELIMINARY; PRT; 42 AA.

AC Q70BW1; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Fatty acid hydroxylase (Fragment).

GN Name=CYP4A24;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Lundell K.;

RT "The porcine taurochenodeoxycholic acid galpha-hydroxylase (CYP 4A21)

RT gene: evolution by gene duplication and gene conversion.";

RL Biochem. J. 378:1053-1058(2004).

RN [2]

RP SEQUENCE FROM N.A.

RA Lundell K.L.;

RT Submitted (Oct-2003) to the EMBL/Genbank/DBJ databases.

DR EMBL; AJ586860; CAB52547.1; -.

FT NON_TER 42

SQ SEQUENCE 42 AA; 4513 MW; 1988CE9A17371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLL 10
 Db 18 LGGLLLL 24

RESULT 55

Q70BW2 PRELIMINARY; PRT; 42 AA.

AC Q70BW2; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Taurochenodeoxycholic 6 alpha-hydroxylase (Fragment).

GN Name=CYP4A21;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Lundell K.;

RT "The porcine taurochenodeoxycholic acid galpha-hydroxylase (CYP 4A21)

RT gene: evolution by gene duplication and gene conversion.";

RL Biochem. J. 378:1053-1058(2004).

RN [2]

RP SEQUENCE FROM N.A.

RA Lundell K.L.;

RT Submitted (Oct-2003) to the EMBL/Genbank/DBJ databases.

DR EMBL; AJ586859; CAB52546.1; -.

FT NON_TER 42

SQ SEQUENCE 42 AA; 4560 MW; 05642E7407371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLLL 10

Db 18 LIGLILL 24

RESULT 56
ID CAES2546 PRELIMINARY; PRT; 42 AA.
AC CAES2546; (TREMBlrel. 27, Created)
DT 03-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 03-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Taurochenodeoxycholic 6 alpha-hydroxylase (Fragment).
GN CYP4A21.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundell K.;
RT "The porcine taurochenodeoxycholic acid 6alpha-hydroxylase (CYP 4A21) gene: evolution by gene duplication and gene conversion.";
RL Biochem. J. 378:1053-1058(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Lundell K.L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ586859; CAES2546.1; -.
FT NON_TER 42
SQ SEQUENCE 42 AA; 4560 MW; 05642E7407371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 LIGLILL 10

RESULT 57
ID CAES2547 PRELIMINARY; PRT; 42 AA.
AC CAES2547; (TREMBlrel. 27, Created)
DT 03-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 03-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Fatty acid hydroxylase (Fragment).
GN CYP4A24.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundell K.;
RT "The porcine taurochenodeoxycholic acid 6alpha-hydroxylase (CYP 4A21) gene: evolution by gene duplication and gene conversion.";
RL Biochem. J. 378:1053-1058(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Lundell K.L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ586860; CAES2547.1; -.
FT NON_TER 42
SQ SEQUENCE 42 AA; 4513 MW; 1988CE9A17371985 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 LIGLILL 10

Db 18 LIGLILL 24

RESULT 58
ID Q9UN20 PRELIMINARY; PRT; 44 AA.
AC Q9UN20; (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Fc gamma receptor III-A (Fragment).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Song Y.W., Hong K.M., Shin C.H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162790; AAD48438.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 44 AA; 5003 MW; 0A7B2538B46395DF CRC64;

Query Match 2.2%; Score 7; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 205 DSGSYFC 211

Db 18 DSGSYFC 24

RESULT 59
ID Q8U2N4 PRELIMINARY; PRT; 66 AA.
AC Q8U2N4; (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein PF0799.
GN OrderedLocName=PF0799;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 3638;
RX MEDLINE=21079003; PubMed=11210495;
RA Robb F.T., Maeder D.L., Brown J.R., DiRuggiero J., Stump M.D., Yeh R.K., Weiss R.B., Dunn D.M.;
RT "Genomic sequence of hyperthermophile, Pyrococcus furiosus: implications for physiology and enzymology.";
RL Meth. Enzymol. 330:134-157(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AEO10196; AAL80923.1; -.
DR HSSP; P11759; IMF2.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002025; NAD BS.
DR InterPro; IPR001732; UDPG_MGDP_dh.
DR Pfam; PF03721; UDPG_MGDP_dh_N; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 66 AA; 7127 MW; B5742284CF9E7FDE CRC64;

Query Match 2.2%; Score 7; DB 2; Length 66;

Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 AVIADSG 207
|||||
Db 21 AVIADSG 27

RESULT 60

072H08 PRELIMINARY; PRT; 70 AA.
AC 072H08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=TTIC1687;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.,
RT "The genome sequence of the extreme thermophile Thermus
thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AB017306; AAS82029.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 70 AA; 7957 MW; 33C85B32786D2144 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 16 LIGLILL 22

RESULT 61

AAS82029 PRELIMINARY; PRT; 70 AA.
AC AAS82029;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN TTIC1687.
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.,
RT "The genome sequence of the extreme thermophile Thermus
thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AB017306; AAS82029.1; -;
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7957 MW; 33C85B32786D2144 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 97;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 16 LIGLILL 22

RESULT 62

08TE42 PRELIMINARY; PRT; 77 AA.
AC 08TE42;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Truncated steroid 21-hydroxylase (EC 1.14.99.10).
GN Name=CYP21,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21601921; PubMed=11739456;
RA Lau I.F., Soardi F.C., Lemos-Martini S.H., Guerra-Jr G., Baptista M.T.,
RA de Mello M.P.;
RT "H28-C insertion in the CYP21 gene: a novel frameshift mutation in a
deficiency.";
RL J. Clin. Endocrinol. Metab. 86:5877-5880(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Lau I.F.;
RT "Novel Mutations in CYP21 Gene."
RL Thesis (2000), Department of Institute of Biological Sciences,
Campinas State University, Campinas, SP, Brazil.
RN [3]
RP SEQUENCE FROM N.A.
RA de Mello M.P.;
RL Submitted (FE8-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; A431212; CND24050.1; -;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004509; F:steroid 21-monooxygenase activity; IEA.
KW Oxidoreductase.
SQ SEQUENCE 77 AA; 8364 MW; ABAFFP3692422B9C CRC64;

Query Match 2.2%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 3 LIGLILL 9

RESULT 63

07U23 PRELIMINARY; PRT; 85 AA.
AC 07U23;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=RB3559;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heltmann K., Rabus R.,

RA Schleener H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planktonic ciliate *Pirellula* sp.
 RL strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294139; CAD733261.1;
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 85 AA; 9616 MW; 797D3DA4F0299FE9 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LKTKTE 242
 |||||
 Db 18 LKTKTE 24

RESULT 64

08FEV3 PRELIMINARY; PRT; 88 AA.
 AC 08FEV3;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE GnsB protein.
 GN OrderedLocustNames=c3176;
 OS *Escherichia coli* O6;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 CX NCBI_TaxID=217992;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=06:HI / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 Rayko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RT Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RA "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic *Escherichia coli*."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 DR EMBL; AE016765; AAN81628.1; -.
 KW Complete proteome.

SQ SEQUENCE 88 AA; 10413 MW; 238B8BD4501BF CRC64;

Query Match 2.2%; Score 7; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 LKTKTE 243
 |||||
 Db 37 LKTKTE 43

RESULT 65

08KAN9 PRELIMINARY; PRT; 92 AA.

AC 08KAN9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Initiate factor 3.2.
 GN Name=Oosp1; Synonym=IF3 2;
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2222142; PubMed=12237121;
 RA Mano H., Nakatani S., Aoyagi R., Ishii R., Iwai Y., Shinoda N.,
 RA Juncho Y., Hura H., Hirose M., Mochizuki C., Yuri M., Im R.-H.,
 RA Funada-Wada U., Wada M.;

RT "IF3, a novel cell-differentiation factor, highly expressed in the
 RT murine liver and ovary."
 RL Biochem. Biophys. Res. Commun. 297:323-328 (2002).
 DR EMBL; AB086437; BAC11848.1; -.
 DR MGI; MGI:2149290; Oosp1.
 SQ SEQUENCE 92 AA; 10597 MW; FC458C6E1005FDA CRC64;

Query Match 2.2%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLGLLL 10
 |||||
 Db 7 LLGLLL 13

RESULT 66

083JUS PRELIMINARY; PRT; 95 AA.
 AC 083JUS;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=EP1833;
 OS *Enterococcus faecalis* (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 CX NCBI_TaxID=1351;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=2250857; PubMed=12663927; DOI=10.1126/science.1080613;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L.A., Binkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
 RA Khouir H.M., Uetreback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
 RA Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT *Enterococcus faecalis*."
 RL Science 299:2071-2074 (2003).
 DR EMBL; AE016952; AAC81598.1; -.
 DR TIGR; EP1833; -.
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 95 AA; 10386 MW; 479FF39F72B99EB CRC64;

Query Match 2.2%; Score 7; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLGLLL 10
 |||||
 Db 36 LLGLLL 42

RESULT 67

016755 PRELIMINARY; PRT; 97 AA.

AC 016755;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Steroid 21-monooxygenase (BC 1.14.99.10) (Fragment).
 GN Name=CYP21A/CYP21B fusion gene;
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood;
 RX MEDLINE=92297162; PubMed=1605859;

RA Helmborg A., Tabarelli M., Fuchs M.A., Keller E., Dobler G.,
 RA Schlegel I., Knorr D., Albert E., Kofer R.,
 RT "Identification of molecular defects causing congenital adrenal
 RT hyperplasia by cloning and differential hybridization of polymerase
 RT chain reaction-amplified 21-hydroxylase (CYP21) genes."
 RL DNA Cell Biol. 11:359-368(1992).
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; X58908; CAA41711.1; -.
 DR PIR; S26485; S26485.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0004509; F:steroid 21-monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002401; EP4501.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PRO0463; EP4501.
 KM Heme; Monooxygenase; Oxidoreductase.
 F7 NON_TER
 F7 SEQUENCE 97 AA; 11069 MW; 84A118F6680C6737 CRC64;
 SQ

Query Match 2.2%; Score 7; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 Db 3 LIGLILL 9

RESULT 68

ID Q8G66 PRELIMINARY; PRT; 97 AA.

AC Q8G66;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative V-SNARE ALVT1b (At1g26670).
 GN Name=At1g26670/T24P13.20;
 GN Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Huan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.C., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK18409; BAC43018.1; -.
 DR EMBL; BT004676; AA042922.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006886; P:intracellular protein transport; IEA.
 DR InterPro; IPR007705; V-SNARE.
 DR Pfam; PF05008; V-SNARE; 1.
 SQ SEQUENCE 97 AA; 11149 MW; 41AAA73C1DCC730 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 AIIILIS 292
 |||||

Db 86 AIIILIS 92

RESULT 69

ID Q950L7 PRELIMINARY; PRT; 98 AA.

AC Q950L7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NADH dehydrogenase subunit 4L (EC 1.6.5.3).
 GN Name=nad4L;
 OS Rhizophidium sp. 136.
 OG Mitochondrion.
 OC Eukaryota; Fungi; Chytridiomycota; Chytridiales; Chytridiaceae;
 OC Rhizophidium.
 OX NCBI_TaxID=60187;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=136;
 RX MEDLINE=21651207; PubMed=11861890;
 RA Forget L., Uetlinova J., Wang Z., Huss V.A.R., Lang B.F.,
 RT "Hydrophidium curvatum: a linear mitochondrial genome, tRNA editing,
 RT and an evolutionary link to lower fungi."
 RL Mol. Biol. Evol. 19:310-319(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=136;
 RA Lang B.F.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040306; AAK84291.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
 DR GO; GO:001491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
 DR InterPro; IPR001133; Oxidored_4L.
 DR InterPro; IPR001324; Oxidored_4L.
 DR Pfam; PF00420; Oxidored_42; 1.
 DR ProDom; PD000359; Oxidred4L; 1.
 KM Mitochondrion; Oxidoreductase.
 SQ SEQUENCE 98 AA; 10822 MW; BF4784F2D7BC5FC CRC64;

Query Match 2.2%; Score 7; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 IILILSL 293
 Db 35 IILILSL 41

RESULT 70

ID Q8QG55 PRELIMINARY; PRT; 100 AA.

AC Q8QG55;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Chemokine ah189 (Macrophage inflammatory protein 3alpha).
 GN Name=MP-3alpha;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655115; PubMed=11797102;
 RA Hughes S., Haynes A., O'Regan M., Bunstead N.,
 RT "Identification, mapping, and phylogenetic analysis of three novel
 RT chicken CC chemokines."
 RL Immunogenetics 53:674-683(2001).
 RN [2]


```

RP SEQUENCE FROM N.A.
RA Hughes S.M., Burnstead N.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn H-B15; TISSUE=Spleen;
RA Sayed A., Horuchi H., Furusawa S., Matsuda H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn H-B15; TISSUE=Spleen;
RA Sayed A.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037861; AAK84434.1; -.
DR EMBL; AB101005; BACS5967.1; -.
DR HSSP; P78556; IM8A.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00139; SCY; 1.
SQ SEQUENCE 100 AA; 1149 MW; BE4F16809FCBE778 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGULLL 10
Db 14 LGULLL 20

RESULT 71
ID YGVA YEAST STANDARD; PRT; 101 AA.
AC P53089;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 11.4 kDa protein in FOX1-KEX1 intergenic region.
GN OederelocusNames=YGL204C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Bjournson A.J., McReynolds A.D.K., Wright L.F.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 272726; CAA96916.1; -.
DR PIR; S64322; S64322.
DR GerMOnline; 141352; -.
DR SGD; S0003172; YGL204C.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 20 40 Potential.
FT TRANSMEM 59 79 Potential.
SQ SEQUENCE 101 AA; 11351 MW; 695B5D009E211566 CRC64;

Query Match 2.2%; Score 7; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGULLL 11
Db 5 LGULLL 11

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Db 33 LGULLL 39

RESULT 72
ID AAS56831 PRELIMINARY; PRT; 101 AA.
AC AAS56831;
DT 25-MAR-2004 (TREMBLrel. 27, Created)
DT 25-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE YGL204C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzalez L., Vasconcelos A.T., Simpson A., Koldner R., Harlow E.,
RA Labaer J.;
RT "Creation of the YPLex clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY58505; AAS56831.1; -.
SQ SEQUENCE 101 AA; 11351 MW; 695B5D009E211566 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGULLL 11
Db 33 LGULLL 39

RESULT 73
ID PLF4 RAT STANDARD; PRT; 105 AA.
AC P06765;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Platelet factor 4 precursor (PF-4) (CXCL4).
GN Name=PF4; Synonyms=Scyb4;
OS Rattus norvegicus (Rat).
OC Baktaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87144263; PubMed=3821732;
RA Dot T., Greenberg S.M., Rosenberg R.D.;
RT "Structure of the rat platelet factor 4 gene: a marker for
RT megakaryocyte differentiation.";
RL Mol. Cell. Biol. 7:898-904(1987).
RN [2]
RP O-GLYCOSYLATION.
RX MEDLINE=94307262; PubMed=8033893;
RA Ravanat C., Gachet C., Herbert J.-M., Schuhler S., Guillemot J.-C.,
RA Usablaiga F., Picard C., Ferrara P., Freund M., Cazenave J.-P.;
RT "Rat platelets contain glycosylated and non-glycosylated forms of
RT platelet factor 4. Identification and characterization by mass
RT spectrometry.";
RL Eur. J. Biochem. 223:303-310(1994).
CC -1- FUNCTION: Platelet factor 4, noncovalently bound to a proteoglycan
CC molecule, is released during platelet aggregation. PF4 neutralizes
CC the anticoagulant effect of heparin because it binds more strongly
CC to heparin than to the chondroitin-4-sulfate chains of the carrier
CC molecule. Chemotactic for neutrophils and monocytes.
CC -1- SUBUNIT: Homotetramer.

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-linked glycan consists of gal-galNAc disaccharide which is
CC modified with sialic acid residues (microheterogeneity).
CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M15254; AAA41832.1; -.
CC PIR: A26774; A26774.
CC HSSP: P02776; IRHP.
CC DR GO: GO:0005576; C:extracellular; ISS.
CC DR GO: GO:0008009; F:chemokine activity; ISS.
CC DR GO: GO:0008201; F:heparin binding; ISS.
CC DR GO: GO:0019221; P:cytokine and chemokine mediated signaling p. .; ISS.
CC DR GO: GO:0030595; P:immune cell chemotaxis; ISS.
CC DR GO: GO:0016525; P:negative regulation of angiogenesis; ISS.
CC DR GO: GO:0045653; P:negative regulation of megakaryocyte differ. .; ISS.
CC DR GO: GO:0030168; P:platelet activation; ISS.
CC DR InterPro: IPR002473; C-X-C/Interlkn_8.
CC DR InterPro: IPR001811; Chemokine_Ilt8.
CC DR InterPro: IPR001089; CXC_chemokine_ilt8.
CC DR Pfam: PF00048; Ilt8; 1.
CC DR PRINTS: PR00436; INTERLEUKIN8.
CC DR PRINTS: PR00437; SMALLCYTCKXC.
CC DR SMART: SM00139; SCY; 1.
CC DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
CC KM Chemotaxis; Cytokine; Glycoprotein; Heparin-binding; Platelet; Signal.
CC FT SIGNAL 1 29
CC FT CHAIN 30 105 Platelet factor 4.
CC FT DISULFID 44 71 By similarity.
CC FT DISULFID 46 87 By similarity.
CC FT CARBOHYD 31 31 O-linked (GalNAc...); partial.
CC SQ SEQUENCE 105 AA; 11286 MW; D9CCND26A284496 CRC64;

Query Match 2.2%; Score 7; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGGLLL 10
Db 18 LGGLLL 24

RESULT 74
Q70HT8 PRELIMINARY; PRT; 105 AA.
AC Q70HT8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE V1ha protein (Fragment).
GN Name=V1ha;
OS Mycoplasma synoviae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2109;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K4;
RA Hammond P.P., Hazel K., Bradbury J.M., Morrow C.J.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B133-99-5;
RA Hammond P.P., Bradbury J.M., Ramirez A.S., Morrow C.J.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ580984; CAE45731.1; -.

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DR EMBL; AJ580983; CAE45730.1; -.
DR InterPro: IPR002988; GA.
DR Pfam: PF01468; GA; 1.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 10464 MW; 4BC03E36A1421D67 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LKTKTEA 243
Db 86 LKTKTEA 92

RESULT 75
CAE45730 PRELIMINARY; PRT; 105 AA.
AC CAE45730;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE V1ha protein (Fragment).
GN V1ha.
OS Mycoplasma synoviae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2109;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B133-99-5;
RA Hammond P.P., Bradbury J.M., Ramirez A.S., Morrow C.J.;
RT "Combined detection and identification of Mycoplasma synoviae strains
RT by amplification of a conserved part of the V1ha gene."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ580983; CAE45730.1; -.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 10464 MW; 4BC03E36A1421D67 CRC64;

Query Match 2.2%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LKTKTEA 243
Db 86 LKTKTEA 92

Search completed: January 4, 2005, 07:02:43
Job time : 122 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 06:58:59 ; Search time 27 Seconds
(without alignments)
1143.910 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 321
Sequence: 1 MGILLGILLGHLTVDTGR.....AYIMLCRKTSQGEHYEAR 321

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.5	124	2	epididymis-specific
2	8	2.5	223	2	hypothetical prote
3	8	2.5	412	2	hypothetical prote
4	8	2.5	667	2	OS-9 protein precu
5	7	2.2	33	2	benzphetamine N-de
6	7	2.2	43	2	collagen alpha 1(I
7	7	2.2	97	4	cytochrome P450 21
8	7	2.2	101	2	probable membrane
9	7	2.2	105	2	platelet factor 4
10	7	2.2	116	2	ig kappa chain pre
11	7	2.2	117	1	ig kappa chain pre
12	7	2.2	117	1	ig kappa chain pre
13	7	2.2	117	2	ig kappa chain pre
14	7	2.2	117	2	ig kappa chain pre
15	7	2.2	117	2	ig kappa chain V r
16	7	2.2	117	2	ig kappa chain V r
17	7	2.2	117	2	ig kappa chain V r
18	7	2.2	117	2	ig kappa chain pre
19	7	2.2	117	2	ig kappa chain pre
20	7	2.2	117	2	ig kappa chain pre
21	7	2.2	117	2	ig kappa chain V r
22	7	2.2	117	2	ig kappa chain pre
23	7	2.2	117	2	ig kappa chain pre
24	7	2.2	117	2	ig kappa chain V r
25	7	2.2	117	2	ig kappa chain V r
26	7	2.2	120	2	ig kappa chain V-J
27	7	2.2	122	2	ig kappa chain V-J
28	7	2.2	122	2	ig kappa chain - h
29	7	2.2	122	2	ig kappa chain - h

30	7	2.2	123	2	S40331	ig kappa chain - h
31	7	2.2	123	2	S40313	ig kappa chain V-J
32	7	2.2	123	2	S40354	ig kappa chain - h
33	7	2.2	124	2	S40318	ig kappa chain V r
34	7	2.2	124	2	S40336	ig kappa chain V-J
35	7	2.2	124	2	S40348	ig kappa chain V-J
36	7	2.2	125	2	S04936	ig kappa chain pre
37	7	2.2	125	2	S40353	ig kappa chain V-J
38	7	2.2	125	2	S40333	ig kappa chain V-J
39	7	2.2	125	2	S40316	ig kappa chain - h
40	7	2.2	125	2	S40349	ig kappa chain V-J
41	7	2.2	125	2	S40315	ig kappa chain - h
42	7	2.2	126	2	E70420	NADH2 dehydrogenas
43	7	2.2	126	2	S40335	ig kappa chain V-J
44	7	2.2	127	2	S40367	ig kappa chain V-J
45	7	2.2	127	2	S11240	ig kappa chain V r
46	7	2.2	127	2	A23986	ig kappa chain pre
47	7	2.2	128	2	S46372	ig light chain var
48	7	2.2	129	1	K1HMDI	ig kappa chain pre
49	7	2.2	129	1	K1HMK	ig kappa chain pre
50	7	2.2	129	2	S52789	ig kappa chain V r
51	7	2.2	129	2	S52792	ig kappa chain V r
52	7	2.2	129	2	S40317	ig kappa chain - h
53	7	2.2	129	2	S52793	ig kappa chain V r
54	7	2.2	129	2	S40369	ig kappa chain - h
55	7	2.2	129	2	S40332	ig kappa chain - h
56	7	2.2	130	2	PL0113	ig kappa chain pre
57	7	2.2	130	2	S40368	ig kappa chain - h
58	7	2.2	130	2	S08079	ig kappa chain pre
59	7	2.2	131	2	S40352	ig kappa chain V-J
60	7	2.2	132	2	S38646	ig kappa chain V r
61	7	2.2	132	2	S40334	ig kappa chain - h
62	7	2.2	135	2	S24320	ig kappa chain pre
63	7	2.2	139	2	S40365	ig kappa chain - h
64	7	2.2	141	2	A49134	ig kappa chain V-I
65	7	2.2	141	2	S57086	YAE1 protein - Yea
66	7	2.2	158	2	T45630	hypothetical prote
67	7	2.2	170	2	D95096	hemolysin-related
68	7	2.2	170	2	A97964	conserved hypochet
69	7	2.2	175	2	I53285	glucocorticoid-reg
70	7	2.2	175	2	A53523	endorphine secretor
71	7	2.2	180	2	A10676	probable exported
72	7	2.2	207	2	H84273	flagellin A1 precu
73	7	2.2	229	2	A20969	ig kappa chain pre
74	7	2.2	230	2	S33161	ig kappa chain - s
75	7	2.2	233	1	U00284	Fc gamma (IgG) rec
76	7	2.2	238	2	S75336	hypothetical prote
77	7	2.2	249	2	E72703	probable reductase
78	7	2.2	254	1	JL0107	Fc gamma (IgG) rec
79	7	2.2	256	2	F70812	probable IgM prot
80	7	2.2	265	2	B81229	phosphatidate cycl
81	7	2.2	265	2	T28102	hypothetical prote
82	7	2.2	269	2	T04095	ribonuclease S hom
83	7	2.2	272	2	AC1426	D-alanyl-D-alanine
84	7	2.2	275	2	C89858	conserved hypochet
85	7	2.2	284	2	S27931	Env/V-mp1 fusion p
86	7	2.2	303	2	D83082	probable permease
87	7	2.2	305	2	C83775	ABC transporter (A
88	7	2.2	309	2	B49698	transcription regu
89	7	2.2	317	2	T39206	hypothetical prote
90	7	2.2	327	2	G90139	deacetylase, proba
91	7	2.2	327	2	AG0870	hypothetical prote
92	7	2.2	340	2	AB2982	ABC transporter, m
93	7	2.2	341	2	AG0195	probable exported
94	7	2.2	344	2	AD1200	conserved hypochet
95	7	2.2	344	2	T24053	hypothetical prote
96	7	2.2	350	2	T29409	hypothetical prote
97	7	2.2	360	2	E82442	probable peptide A
98	7	2.2	360	2	F98301	hypothetical prote
99	7	2.2	372	1	UHHUCN	ciliary neurotroph
100	7	2.2	372	2	I58141	ciliary neurotroph

ALIGNMENTS

RESULT 1

154768

epididymis-specific four-disulfide core protein CE4 - dog
C/Species: Canis lupus familiaris (dog)

C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: I54768

R/Elmerbrock, K.; Pera, I.; Hartung, S.; Ivell, R.

Int. J. Androl. 17, 314-323, 1994

A/Title: Gene expression in the dog epididymis: a model for human epididymal function.

A/Reference number: I54768; MUID:95263175; PMID:7744511

A/Accession: I54768

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-124 <BL>

A/Cross-references: UNIPROT:Q28894; GB:S77395; NID:g945180; PIDN:AA834264.1; PID:g945181
C/Superfamily: antileukoprotease; antileukoprotease repeat homology
F/76-123/Domain: antileukoprotease repeat homology <ALP>

Query Match

Best Local Similarity 2.5%; Score 8; DB 2; Length 124;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILLG 11
|||||

DB 14 LIGLILLG 21

RESULT 2

H83359

hypothetical protein PA2284 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa
C/Date: 13-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: H83359

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lm,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: H83359

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-223 <STO>

A/Cross-references: UNIPROT:Q91101; GB:AE004654; GB:AE004091; NID:g9948311; PIDN:AA60567

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA2284

Query Match

Best Local Similarity 2.5%; Score 8; DB 2; Length 223;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILLG 11
|||||

DB 47 LIGLILLG 54

RESULT 3

A69256

hypothetical protein AF0049 - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: A69256

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Goeayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A/Authors: Ueberback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea

A/Reference number: A69250; MUID:98049343; PMID:939475

A/Accession: A69256

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-412 <ML>

A/Cross-references: UNIPROT:Q30187; GB:AE001103; GB:AE000782; NID:g2689426; PIDN:AA8911

Query Match

Best Local Similarity 2.5%; Score 8; DB 2; Length 412;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 YIGETISAG 277
|||||

DB 142 YIGETISAG 149

RESULT 4

JC5889

OS-9 protein precursor - human

N/Contains: OS-9 protein, splice form 1; OS-9 protein, splice form 2; OS-9 protein, spli

C/Species: Homo sapiens (man)

C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004

C/Accession: JC5889; J0106; J0107; J0108

R/Kimura, Y.; Nakazawa, M.; Tsuchiya, N.; Asakawa, S.; Shimizu, N.; Yamada, M.

J. Biochem. 122, 1190-1195, 1997

A/Title: Genomic organization of the OS-9 gene amplified in human sarcomas.

A/Reference number: JC5889; MUID:98158329; PMID:9498564

A/Accession: JC5889

A/Molecule type: DNA

A/Residues: 1-667 <KIM1>

A/Cross-references: UNIPROT:Q13438; DDBJ:AB002806; NID:g2780782; PIDN:BAA24363.1; PID:dl

A/Experimental source: sarcomas

A/Note: neither the complete nucleic acid sequence nor the complete translation are sho

R/Kimura, Y.; Nakazawa, M.; Yamada, M.

J. Biochem. 123, 876-882, 1998

A/Title: Cloning and characterization of three isoforms of OS-9 cDNA and expression of t

A/Reference number: J0108; MUID:98230694; PMID:9562620

A/Accession: J0106

A/Molecule type: mRNA

A/Residues: 1-667 <KIM2>

A/Cross-references: DDBJ:AB002806; NID:g2780782; PIDN:BAA24363.1; PID:dl025275; PID:g278

A/Accession: J0107

A/Molecule type: mRNA

A/Residues: 1-534,590-667 <KIM3>

A/Cross-references: DDBJ:AB002806

A/Accession: J0108

A/Molecule type: mRNA

A/Residues: 1-455,471-534,590-667 <KIM4>

A/Cross-references: DDBJ:AB002806

C/Comment: This protein is involved in amplification and overexpression of various tumor

C/Genetics:

A/Gene: OS-9

A/Cross-references: GDB:9958646

A/Map position: 12q13-12q15

C/Keywords: alternative splicing; carcinogenesis; glycoprotein

F/1-25/Domain: signal sequence #status predicted <Sig>

F/26-667/Product: OS-9 protein, splice form 1 #status predicted <MAT1>

F/26-534,590-667/Product: OS-9 protein, splice form 2 #status predicted <MAT2>

F/26-455,471-534,590-667/Product: OS-9 protein, splice form 3 #status predicted <MAT3>

F/177/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 2.5%; Score 8; DB 2; Length 667;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILLG 11
|||||

DB 10 LIGLILLG 17

RESULT 5

A3154

benzphetamine N-demethylase (EC 1.14.14.-) cytochrome P450 2B - guinea pig (fragment)

N/Alternate names: cytochrome P450(GP-1)
 C/Species: *Cavia porcellus* (guinea pig)
 C/Date: 31-Mar-1992 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
 C/Accession: S15135; S28205; A36154
 R/Oguri, K.; Kaneko, H.; Tanimoto, Y.; Yamada, H.; Yoshimura, H.
 Arch. Biochem. Biophys. 287, 105-111, 1991
 A/Title: A constitutive form of guinea pig liver cytochrome P450 closely related to phenanthrene hydroxylase
 A/Reference number: S15135; MUID:91378363; PMID:1897986
 A/Accession: S15135
 A/Molecule type: protein
 A/Residues: 1-33 <ARC>
 A/Cross-references: UNIPROT:Q9QVJ4
 R/Yamada, H.; Kaneko, H.; Takeuchi, K.; Oguri, K.; Yoshimura, H.
 Arch. Biochem. Biophys. 299, 248-254, 1992
 A/Title: Tissue-specific expression, induction, and inhibition through metabolic interme
 A/Reference number: S28205; MUID:91079373; PMID:1444463
 A/Accession: S28205
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-31 <YAM>
 R/Narimatsu, S.; Akutsu, Y.; Matsunaga, T.; Watanabe, K.; Yamamoto, I.; Yoshimura, H.
 Biochem. Biophys. Res. Commun. 172, 607-613, 1990
 A/Title: Purification of a cytochrome P450 isozyme belonging to a subfamily of P450 IIB
 A/Reference number: A36154; MUID:91054472; PMID:2173574
 A/Accession: A36154
 A/Molecule type: protein
 A/Residues: 1-20 <NAR>
 A/Genetics:
 C/Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C/Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Query Match 2.2%; Score 7; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLLLL 10
 Db 12 LGLLLL 18

RESULT 6
 S13581
 collagen alpha 1(IX) chain precursor, short splice form - human (fragment)
 C/Species: *Homo sapiens* (man)
 C/Date: 21-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 15-Sep-2003
 C/Accession: S13581; D35980
 R/Muragaki, Y.; Kimura, T.; Nimomiya, Y.; Olsen, B.R.
 Eur. J. Biochem. 192, 703-708, 1990
 A/Title: The complete primary structure of two distinct forms of human alpha-1(IX) colla
 A/Reference number: S13580; MUID:9106164; PMID:2209617
 A/Accession: S13581
 A/Molecule type: mRNA
 A/Residues: 1-43 <MUR>
 A/Cross-references: EMBL:X54413; NID:930087; PIN:CA38277.1; PID:930088
 R/Muragaki, Y.; Nimomiya, I.; Henney, A.; Nimomiya, Y.; Olsen, B.R.
 Proc. Natl. Acad. Sci. U.S.A. 87, 2400-2404, 1990
 A/Title: The alpha 1(IX) collagen gene gives rise to two different transcripts in both m
 A/Reference number: A35980; MUID:90207204; PMID:1690866
 A/Accession: D35980
 A/Molecule type: DNA
 A/Residues: 1-24 <MUR>
 A/Cross-references: EMBL:M32133
 C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 C/Genetics:
 A/Genes: GDB:COL9A1
 A/Cross-references: GDB:119794; OMIM:120210
 A/Map position: 6q12-6q14
 A/Intons: 24/3
 C/Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2
 C/Function:
 A/Description: structural component of extracellular fibrous polymer associated with type

A/Note: in corneal epithelium the short splice form is predominantly produced
 C/Keywords: alternative splicing; coll; cornea; extracellular matrix; glycoprote
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-43/Product: collagen alpha 1(IX) chain, short splice form (fragment) #status predi
 F/24-25/Domain: non-collagenous NC4 #status predicted <NC4>
 F/26-43/Domain: collagenous COL3 (fragment) #status predicted <COL3>
 F/2/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte

Query Match 2.2%; Score 7; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGLLLL 11
 Db 11 LGLLLL 17

RESULT 7
 S26485
 cytochrome P450 21A/B mutant fusion protein - human
 N/Alternate names: steroid 21-monooxygenase
 C/Species: *Homo sapiens* (man)
 C/Date: 06-Jan-1995 #sequence_revision 17-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S26485; S29672
 R/Helmsberg, A.; Kofler, R.
 submitted to the EMBL Data Library, March 1991
 A/Reference number: S26484
 A/Accession: S26485
 A/Molecule type: DNA
 A/Residues: 1-97 <HEL>
 A/Cross-references: UNIPROT:Q16755; EMBL:X58901
 A/Experimental source: leukocyte clone AGS 8-23
 A/Note: an unequal cross-over mutation of the CYP21P pseudogene and CYP21 gene in a con
 A/Accession: S29672
 A/Molecule type: DNA
 A/Residues: 1-97 <HR2>
 A/Cross-references: EMBL:X58908
 C/Genetics:
 A/Genes: CYP21P/CYP21
 A/Map position: 6p21.3
 A/Intons: 68/1
 C/Keywords: fusion protein

Query Match 2.2%; Score 7; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGLLLL 10
 Db 3 LGLLLL 9

RESULT 8
 S64222
 probable membrane protein YGL204C - yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: hypothetical protein G1234
 C/Species: *Saccharomyces cerevisiae*
 C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
 C/Accession: S64222
 R/Bourneon, A.J.; McReynolds, A.D.; K.; Wright, L.F.
 submitted to the Protein Sequence Database, May 1996
 A/Reference number: S64218
 A/Accession: S64222
 A/Molecule type: DNA
 A/Residues: 1-101 <BOU>
 A/Cross-references: UNIPROT:P53089; EMBL:Z72726; NID:G1322837; PID:G1322838; GSPDB:GN00
 C/Experimental source: strain S288C
 C/Genetics:
 A/Genes: YGL204C
 A/Cross-references: SGD:S0003172
 A/Map position: 7L
 C/Superfamily: *Saccharomyces* probable membrane protein YGL204C
 C/Keywords: transmembrane protein

F:22-38/Domain: transmembrane #status predicted <TM1>
F:60-76/Domain: transmembrane #status predicted <TM2>

Query Match

2.2%; Score 7; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LGILLG 11

|||||

DB 33 LGILLG 39

RESULT 9

A26774 Platelet factor 4 precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004

C/Accession: A26774; S45657

R/Dol, T./ Greenberg, S.M.; Rosenberg, R.D.

Mol. Cell. Biol. 7, 898-904, 1987

A/Title: Structure of the rat platelet factor 4 gene: a marker for megakaryocyte differ

A/Reference number: A26774; MUID:87144262; PMID:3821732

A/Accession: A26774

A/Molecule type: DNA, mRNA

A/Residues: 1-105 <DOI>

A/Cross-references: UNIPROT:P06765; GB:M15254; NID:9206090; PIDN:AAA41832.1; PID:9206091

R/Ravanat, C./ Gacher, C.; Herbert, J.M.; Schuhler, S.; Guillemet, J.C.; Uzabias, F.; F

Eur. J. Biochem. 223, 203-210, 1994

A/Title: Rat platelets contain glycosylated and non-glycosylated forms of platelet facto

A/Reference number: S45657; MUID:94307262; PMID:8033893

A/Accession: S45657

A/Molecule type: protein

A/Residues: 30-42 <RAV>

C/Superfamily: beta-thromboglobulin

Query Match

2.2%; Score 7; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGILLG 10

|||||

DB 18 LGILLG 24

RESULT 10

A27594

Ig kappa chain precursor V-I region (NaIn-6) - human

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000

C/Accession: A27594

R/Graninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Korsmeyer, S.J.

J. Exp. Med. 167, 488-501, 1988

A/Title: The kappa-deleting element. Germ-line and rearranged, duplicated and dispersed f

A/Reference number: A92779; MUID:86154735; PMID:3126251

A/Accession: A27594

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-116 <GRA>

A/Note: this sequence was translated from an aberrantly rearranged kappa gene from lambd

C/Genetics:

A/Map position: 2

A/Intons: 19/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-22/Domain: signal sequence #status predicted <SIG>

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match

2.2%; Score 7; DB 2; Length 116;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGILLG 10

|||||

DB 9 LGILLG 15

RESULT 11

KIHU12

Ig kappa chain precursor V-I region (HK101) - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004

C/Accession: A01881; A21056

R/Bentley, D.L.; Rabbits, T.H.

Nature 288, 730-733, 1980

A/Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa gene

A/Reference number: A93241; MUID:81098966; PMID:6779204

A/Accession: A01881

A/Molecule type: DNA

A/Residues: 1-117 <BEN1>

A/Cross-references: UNIPROT:P01601; GB:V00558; GB:J00244; GB:J00246; NID:933176; PIDN:C

A/Note: the sequence was determined from the germline gene

R/Bentley, D.L.; Rabbits, T.H.

Cell 32, 181-189, 1983

A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplica

A/Reference number: A21056; MUID:83129397; PMID:6402305

A/Accession: A21056

A/Molecule type: DNA

A/Residues: 1-117 <BEN2>

A/Cross-references: GB:K01322; NID:9185993; PIDN:AAA8930.1; PID:9185994

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

A/Intons: 19/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>

F:38-112/Domain: immunoglobulin homology <IMM>

F:45-110/Disulfide bonds: #status predicted

Query Match

2.2%; Score 7; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LGILLG 10

|||||

DB 9 LGILLG 15

RESULT 12

KIHU12

Ig kappa chain precursor V-I region (HK102) - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004

C/Accession: A01882

R/Bentley, D.L.; Rabbits, T.H.

Nature 288, 730-733, 1980

A/Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa gene

A/Reference number: A93241; MUID:81098966; PMID:6779204

A/Accession: A01882

A/Molecule type: DNA

A/Residues: 1-117 <BEN3>

A/Cross-references: UNIPROT:P01602; GB:J00245; NID:9185981; PIDN:AAA59087.1; PID:9185982

A/Note: the sequence was determined from the germline gene

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

A/Intons: 19/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-117/Product: Ig kappa chain V-I region (HK102) #status predicted <MAT>
F:38-112/Domain: immunoglobulin homology <IMM>
F:45-110/Distulfide bonds: #status predicted

Query Match 2.2%; Score 7; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
| | | | |
| | | | |
Db 9 LIGLILL 15

RESULT 13

C21056
Ig kappa chain precursor V region (HK137) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000

C/Accession: C21056
R/Huber, D.L.; Rabbitts, T.H.

Cell 32; 181-189, 1983

A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated

A/Reference number: A21056; MUID:83129397; PMID:6402305

A/Accession: C21056

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <BBN>

A/Cross-references: GB:J00248; NID:G185991; PIDN:AAA59094.1; PID:G185992

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
| | | | |
| | | | |
Db 9 LIGLILL 15

RESULT 14

S41811
Ig kappa chain V region L22 - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000

C/Accession: S41811

R/Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zac

Eur. J. Immunol. 23, 2868-2875, 1993

A/Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequenc

A/Reference number: S41809; MUID:94039386; PMID:8223863

A/Accession: S41811

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <HDB>

A/Cross-references: EMBL:X72816; NID:G415368; PIDN:CAA51335.1; PID:G4388773

C/Genetics: 19/1

A/Introns: 19/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
| | | | |
| | | | |
Db 9 LIGLILL 15

RESULT 15

S41812

Ig kappa chain V region L24, allelic sequence - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S41812

R/Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Za

Eur. J. Immunol. 23, 2868-2875, 1993

A/Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen

A/Reference number: S41809; MUID:94039386; PMID:8223863

A/Accession: S41812

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-117 <HDB>

A/Cross-references: EMBL:X72819; NID:G415374; PIDN:CAA51338.1; PID:G415375

C/Genetics: 19/1

A/Introns: 19/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIGLILL 10
| | | | |
| | | | |
Db 9 LIGLILL 15

RESULT 16

S24206
Ig kappa chain V region (Vx O12 and Vx O2) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C/Accession: S24206; S24209

R/Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.

Eur. J. Immunol. 21, 1821-1827, 1991

A/Title: The human immunoglobulin kappa locus. Characterization of the duplicated O reg

A/Reference number: S24205; MUID:91330953; PMID:1907917

A/Accession: S24206

A/Molecule type: DNA

A/Residues: 1-117 <PAR>

A/Cross-references: EMBL:X59315; NID:G33247; PIDN:CAA42002.1; PID:G33248

A/Experimental source: placenta

A/Genetics: G1

A/Accession: S24209

A/Molecule type: DNA

A/Residues: 1-117 <PMW>

A/Cross-references: EMBL:X59312; NID:G33252; PIDN:CAA41999.1; PID:G33253

A/Experimental source: placenta

A/Genetics: G2

C/Genetics: <G1>

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

A/Map position: 2

S42264
Ig kappa chain V region (L11) - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S42264
R/Scott, M.G.; Citrimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A/Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A/Reference number: S42263; MUID:92043792; PMID:1940382
A/Accession: S42264
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-117 <SCO>
A/Cross-references: EMBL:M64858; NID:g185952; PIDN:AAA58924.1; PID:g185953
C/Genetics:
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 18
S11700
Ig kappa chain precursor V-I region - human
C:Species: Homo sapiens (man)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S11700
R/Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A/Title: A large section of the gene locus encoding human immunoglobulin variable region
A/Reference number: S11697; MUID:85264787; PMID:3927006
A/Accession: S11700
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-117 <PEC>
A/Cross-references: EMBL:X17262; NID:g37873; PIDN:CAA5156.1; PID:g296686
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1985
C/Genetics:
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 19
S10227
Ig kappa chain precursor V region (orphan V108) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C/Accession: S10227
R/Huber, C.; Thiebe, R.; Hameister, H.; Smola, H.; Loetscher, E.; Zachau, H.G.
Nucleic Acids Res. 18, 3475-3478, 1990
A/Title: A human immunoglobulin kappa orphan without sequence defects may be the product
A/Reference number: S10227; MUID:90301460; PMID:2114012
A/Accession: S10227
A/Molecule type: DNA
A/Residues: 1-117 <HUB>

A/Cross-references: EMBL:X51887
C/Genetics:
A/Map position: 2q12-q14
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 20
S41809
Ig kappa chain V region A30 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S41809
R/Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Weindl, A.; Thiebe, R.; Iamm, R.; Za
bur, J. Immunol. 23, 2868-2875, 1993
A/Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen
A/Reference number: S41809; MUID:94039386; PMID:8223863
A/Accession: S41809
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-117 <HUB>
A/Cross-references: EMBL:X72808; NID:g415383; PIDN:CAA51328.1; PID:g415384
C/Genetics:
A/Intons: 19/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 21
B21056
Ig kappa chain precursor V region (HK134) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C/Accession: B21056
R/Bentley, D.L.; Rablits, T.H.
Cell 32, 181-189, 1983
A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicat
A/Reference number: A21056; MUID:83129397; PMID:6402305
A/Accession: B21056
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-117 <BEN>
A/Cross-references: GB:K01323; NID:g185995; PIDN:AAA58931.1; PID:g185996
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 22

S21527
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S11699; S34076; S34105; S21521; S21527
R:Peck, M.; Smola, H.; Pohlman, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A:Title: A large section of the gene locus encoding human immunoglobulin variable region
A:Reference number: S11697; MUID:85264787; PMID:3927006
A:Accession: S11699
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <PBC>
A:Cross-references: EMBL:X17263; NID:G37889; PIDN:CAA35167.1; PID:G296687
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
R:Magner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34076
A:Molecule type: DNA
A:Residues: 30-117 <WA2>
A:Cross-references: EMBL:X66044; NID:G33320; PIDN:CAA46843.1; PID:G33321; EMBL:X66043; N
A:Experimental source: patient.7
A:Accession: S34105
A:Molecule type: DNA
A:Residues: 30-117 <WAG>
A:Cross-references: EMBL:X66044; NID:G33320; PIDN:CAA46843.1; PID:G33321
C:Genetics:
A:Insertions: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>
Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LIGLILL 10
DB 9 LIGLILL 15

RESULT 23
S24207
Ig kappa chain V region (Vx 014 and Vx 04) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S24207; S24210
R:Pergent, W.; Meindl, A.; Thiebe, R.; Miltzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated O regi
A:Reference number: S24205; MUID:9130953; PMID:1907917
A:Accession: S24207
A:Molecule type: DNA
A:Residues: 1-117 <PAR>
A:Cross-references: EMBL:X59316
A:Genetics: G1
A:Accession: S24210
A:Molecule type: DNA
A:Residues: 1-117 <PAW>
A:Cross-references: EMBL:X59313
A:Genetics: G2
C:Genetics: <G1>
A:Gene: Vx 014
A:Map position: 2
A:Insertions: 19/1
C:Genetics: <G2>
A:Gene: Vx 04

A:Map position: 2

A:Insertions: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 9 LIGLILL 15

RESULT 24

S41810
Ig kappa chain V region L14 - human
C:Species: Homo sapiens (man)
C:Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S41810
R:Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Za
Eur. J. Immunol. 23, 2868-2875, 1993
A:Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen
A:Reference number: S41809; MUID:94039386; PMID:8223863
A:Accession: S41810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <HUB>
A:Cross-references: EMBL:X63392
C:Genetics:
A:Insertions: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 9 LIGLILL 15

RESULT 25

S42263
Ig kappa chain V region (08) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42263
R:Scott, M.G.; Crichton, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Qu
J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IGG antibody repertoire to Haemophilus in
A:Reference number: S42263; MUID:92043792; PMID:1940382
A:Accession: S42263
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <SCO>
A:Cross-references: EMBL:M64855; NID:G185963; PIDN:AAA58925.1; PID:G185964
A:Genetics:
A:Insertions: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMW>

Query Match 2.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 9 LIGLILL 15

RESULT 26

S46374
Ig kappa chain V-J region (T33-4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46374; S36651
R/Bensimon, C.; Chastagner, P.; Zouali, M.
EMBL J 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
A/Reference number: S46369; MUID:94333975; PMID:80359491
A/Accession: S46374
A/Molecule type: mRNA
A/Residues: 1-120 <RLE>
A/Cross-references: EMBL:Z27175; NID:g415965; PIDN:CAA61699.1; PID:g415966
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||

Db 2 LIGLILL 8

RESULT 27

S40351
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40351
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40351
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RLE>
A/Cross-references: EMBL:X72461; NID:g441390; PIDN:CAA51129.1; PID:g441391
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||

Db 3 LIGLILL 9

RESULT 28

S40314
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40314
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40314
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RLE>
A/Cross-references: EMBL:X72424
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin
F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||

Db 2 LIGLILL 8

RESULT 29

S40370
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40370
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40370
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <RLE>
A/Cross-references: EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PID:g441429
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||

Db 1 LIGLILL 7

RESULT 30

S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <RLE>
A/Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||

Db 3 LIGLILL 9

RESULT 31

S40313
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40313
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40313
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLB>
 A/Cross-references: EMBL:X72423; NID:9441314; PIDN:CAAS1091.1; PID:9441315
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 DB 3 LIGLILL 9

RESULT 32
 S40354
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40354
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40354
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLB>
 A/Cross-references: EMBL:X72464; NID:9441396; PIDN:CAAS1132.1; PID:9441397
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 DB 1 LIGLILL 7

RESULT 33
 S40318
 Ig kappa chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40318
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40318
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLB>
 A/Cross-references: EMBL:X72428; NID:9441324; PIDN:CAAS1096.1; PID:9441325
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 DB 3 LIGLILL 9

RESULT 34
 S40336
 Ig kappa chain V-J region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40336
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40336
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLB>
 A/Cross-references: EMBL:X72446; NID:9441360; PIDN:CAAS1114.1; PID:9441361
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 DB 2 LIGLILL 8

RESULT 35
 S40348
 Ig kappa chain V-J region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40348
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40348
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KLB>
 A/Cross-references: EMBL:X72458; NID:9441384; PIDN:CAAS1126.1; PID:9441385
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LIGLILL 10
 DB 7 LIGLILL 13

RESULT 36
 S04936
 Ig kappa chain precursor V-J region (1H1) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 26-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
 C/Accession: S04936
 R/Levy, S.; Mendel, E.; Kon, S.; Avnur, Z.; Levy, R.
 J. Exp. Med. 168, 475-489, 1988
 A/Title: Mutational hot spots in Ig V region genes of human follicular lymphomae.
 A/Reference number: S04936; MUID:88316166; PMID:3045247
 A/Accession: S04936

A:Molecule type: mRNA
A:Residues: 1-125 <LEU>
A:Cross-references: EMBL:X13076; NID:g33173; PIDN:CAA11477.1; PID:g736243
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F/18-125/Product: Ig kappa chain (fragment) #status predicted <MAT>
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 4 LIGLILL 10

RESULT 37

S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 1 LIGLILL 7

RESULT 38

S40333
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40333
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72443; NID:g441354; PIDN:CA51111.1; PID:g441355
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 5 LIGLILL 11

RESULT 39

S40316
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40316
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40316
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72426
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 2 LIGLILL 8

RESULT 40

S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S40349
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40349
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CA51127.1; PID:g441387
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
DB 4 LIGLILL 10

RESULT 41

S40315
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40315
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40315
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: EMBL:X72425; NID:g441318; PIDN:CA51093.1; PID:g441319
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F,31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
| | | | |
Db 2 LIGLILL 8

RESULT 42

E70420
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoA1 - Aquifex aeolicus
C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: E70420

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; Ok
V.

Nature 392, 353-358, 1998

A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: E70420

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-126 <AQF>

A:Cross-references: UNIPROT:O67392; GB:AE000737; NID:g2983782; PIDN:AA07346.1; PID:g298

A:Experimental source: strain VFS

C:Genetics:

A:Gene: nuoA1

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 3

C:Keywords: membrane-associated complex; NAD: oxidoreductase

Query Match 2.2%; Score 7; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
| | | | |
Db 64 LIGLILL 70

RESULT 43

S40335

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40335

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40335

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-126 <KLE>

A:Cross-references: EMBL:X72445

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F,31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
| | | | |
Db 2 LIGLILL 8

RESULT 44

S40367

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40367

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F,31-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
| | | | |
Db 4 LIGLILL 10

RESULT 45

S11240

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S11240

R;Feigenhauer, M.; Kohl, J.; Rueker, F.

Nucleic Acids Res. 18, 4927, 1990

A>Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A:Reference number: S11239; MUID:90370490; PMID:1697678

A:Accession: S11240

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-127 <FEL>

A:Cross-references: EMBL:X53612; NID:g23868; PIDN:CAA37674.1; PID:g762937

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F,38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
| | | | |
| | | | |
Db 9 LIGLILL 15

RESULT 46

A23986

Ig kappa chain precursor V region (IR162) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 21-Jan-2000
C:Accession: A23986

R;Helman, L.; Engstrom, A.; Bennich, H.; Pettersson, U.

Gene 40, 107-114, 1985

A>Title: Structure and expression of kappa-chain genes in two IgE-producing rat immuno

A:Reference number: A91541; MUID:86137406; PMID:3005117

A:Accession: A23986

A:Molecule type: mRNA

A:Residues: 1-127 <HEL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F,36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 7 LIGLILL 13

RESULT 47

S46372
IG light chain variable region (VJ) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S46372
R/Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBL J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rege
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46372
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <BEN>
A/Cross-references: EMBL:Z27173
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 7 LIGLILL 13

RESULT 48

KIRHDI
Ig kappa chain precursor V-I region (Daudi) - human
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01884
R/Klobeck, H.G.; Combricato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A/Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A/Reference number: A93534; MUID:85014148; PMID:6091049
A/Accession: A01884
A/Molecule type: DNA
A/Residues: 1-129 <KLO>
A/Cross-references: UNIPROT:P04432; GB:K02134; NID:g185821; PID:g185822
A/Note: the sequence was determined from the differentiated gene
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
A/Intons: 19/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-129/Product: Ig kappa chain V-I region (Daudi) #status predicted <MAT>
F/23-129/Region: framework 1
F/23-45/Region: framework 2
F/38-112/Domain: immunoglobulin homology <IMM>
F/46-56/Region: complementarity-determining 1
F/57-71/Region: framework 2
F/72-78/Region: complementarity-determining 2
F/79-110/Region: framework 3
F/111-119/Region: complementarity-determining 3
F/120-129/Region: framework 4
F/45-110/Disulfide bonds: #status predicted

Query Match 2.2%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 49

KIRHMK
Ig kappa chain precursor V-I region (Walker) - human
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01883
R/Klobeck, H.G.; Combricato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A/Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cel
A/Reference number: A93534; MUID:85014148; PMID:6091049
A/Accession: A01883
A/Molecule type: DNA
A/Residues: 1-129 <KLO>
A/Cross-references: UNIPROT:P04431
A/Note: the sequence was determined from the differentiated gene
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>
F/23-129/Region: framework 1
F/38-112/Domain: immunoglobulin homology <IMM>
F/46-56/Region: complementarity-determining 1
F/57-71/Region: framework 2
F/72-78/Region: complementarity-determining 2
F/79-110/Region: framework 3
F/111-119/Region: complementarity-determining 3
F/120-129/Region: framework 4
F/45-110/Disulfide bonds: #status predicted

Query Match 2.2%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
|||||
Db 9 LIGLILL 15

RESULT 50

S52789
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S52789
R/Rocca, A.; Khanlidi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret
submitted to the EMBL Data Library, March 1995
A/Description: Light chain V region gene usage restriction and peculiarities in myeloma
A/Reference number: S52789
A/Accession: S52789
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <ROC>
A/Cross-references: EMBL:X85995; NID:g758588; PID:CA55987.1; PID:g758588
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 51

552792
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S52792
R:Rocca, A.; Khamlich, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52792
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:CROSS-references: EMBL:X85996; NID:G758598; PIDN:CAAS9988.1; PID:G758599
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 52

S40317
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40317
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40317
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:CROSS-references: EMBL:X72427; NID:G441322; PIDN:CAAS1095.1; PID:G441323
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 LIGLILL 10
| | | | |
Db 8 LIGLILL 14

RESULT 53

S52793
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S52793
R:Rocca, A.; Khamlich, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52793

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:CROSS-references: EMBL:X85997; NID:G758600; PIDN:CAAS9989.1; PID:G758601
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 LIGLILL 10
| | | | |
Db 9 LIGLILL 15

RESULT 54

S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:CROSS-references: EMBL:X72479; NID:G441426; PIDN:CAAS1147.1; PID:G441427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 LIGLILL 10
| | | | |
Db 8 LIGLILL 14

RESULT 55

S40332
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40332
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40332
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:CROSS-references: EMBL:X72442; NID:G441352; PIDN:CAAS1110.1; PID:G441353
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 LIGLILL 10
| | | | |
Db 4 LIGLILL 10

RESULT 56
 PL0113
 Ig kappa chain precursor V-I region (CJ) - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
 C/Accession: PL0113
 R/Levy, S.; Mendel, E.; Kon, S.; Avnur, Z.; Levy, R.
 J. Exp. Med. 168, 475-489, 1988
 A/Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.
 A/Reference number: S04936; MUID:88316166; PMID:3045247
 A/Accession: PL0113
 A/Molecule type: mRNA
 A/Residues: 1-130 <LEV>
 A/Experimental source: follicular lymphoma cells
 A/Note: the sequence shown here is derived from the consensus nucleotide sequence of the
 om tumor cells of a single patient
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; hybridoma; immunoglobulin
 F/1-22/Domain: signal sequence #status predicted <SIG>
 F/23-130/Product: Ig kappa chain V-I region CJ #status predicted <MAT>
 F/38-112/Domain: immunoglobulin homology <IMM>
 F/46-56/Region: complementarity-determining 1
 F/72-78/Region: complementarity-determining 2
 F/111-130/Region: complementarity-determining 3
 F/118-130/Region: J1

Query Match 2.2%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 Db 9 LIGLILL 15

RESULT 57
 S40368
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40368
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40368
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-130 <KLB>
 A/Cross-references: EMBL:X72478; NID:G441424; PIDN:CAAS1146.1; PID:G441425
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 Db 4 LIGLILL 10

RESULT 58
 S08079
 Ig kappa chain precursor V-J region (clone VKB95g) - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000
 C/Accession: S08079
 R/Avadi, H.; Cazenave, P.A.; Marche, P.N.
 submitted to the EMBL Data Library, February 1989
 A/Reference number: S08077
 A/Accession: S08079

A/Molecule type: DNA
 A/Residues: 1-130 <AYA>
 A/Cross-references: EMBL:X14364
 C/Genetics: 17/3
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-17/Domain: signal sequence #status predicted <SIG>
 F/18-113/Product: Ig kappa chain (fragment) #status predicted <MAT>
 F/38-113/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 Db 9 LIGLILL 15

RESULT 59
 S40352
 Ig kappa chain V-J-C region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40352
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40352
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-131 <KLB>
 A/Cross-references: EMBL:X72462; NID:G441392; PIDN:CAAS1130.1; PID:G441393
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 Db 7 LIGLILL 13

RESULT 60
 S38646
 Ig kappa chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S38646
 R/Bensimon, C.; Chastagner, P.; Zouali, M.
 submitted to the EMBL Data Library, November 1993
 A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
 A/Reference number: S38643
 A/Accession: S38646
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-132 <BEN>
 A/Cross-references: EMBL:Z7173; NID:G415961; PIDN:CAAS1697.1; PID:G415962
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/40-114/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLILL 10
 Db 4 LIGLILL 10

Db 11 LIGLALL 17

RESULT 61

S40334

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40334

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40334

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-132 <KLE>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLALL 10
|||||
8 LIGLALL 14

RESULT 62

S24320

Ig kappa chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000

C/Accession: S24320

R:Aucuturier, P.; Khamlich, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne,

Biochem. J. 285, 149-152, 1992

A>Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr

A/Reference number: S24319; MUID:92344562; PMID:1379039

A/Accession: S24320

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-135 <AUC>

A/Cross-references: EMBL:X64133; NID:932810; PIDN:CAA45494.1; PID:932811

A/Note: the authors translated the codon CAA for residue 122 as Glu

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLALL 10
|||||
Db 9 LIGLALL 15

RESULT 63

S40365

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40365

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40365

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-139 <KLE>

A/Cross-references: EMBL:X72475; NID:9441418; PIDN:CAA51143.1; PID:9441419

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLALL 10
|||||
Db 2 LIGLALL 8

RESULT 64

A49134

Ig kappa chain V-I region (ISE) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C/Accession: A49134; S25115

R:Rocca, A.; Khamlich, A.A.; Aucuturier, P.; Noel, L.H.; Denotory, L.; Preud'homme, J.

Clin. Exp. Immunol. 91, 506-509, 1993

A>Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in 11g

A/Reference number: A49134; MUID:93185310; PMID:7680298

A/Accession: A49134

A/Status: preliminary

A/Molecule type: mRNA; protein

A/Residues: 1-141 <ROC>

A/Cross-references: EMBL:X67322; NID:933268; PIDN:CAA47736.1; PID:933269

A/Note: sequence extracted from NCBI backbone (NCBI:P:127088)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LIGLALL 10
|||||
Db 9 LIGLALL 15

RESULT 65

S57086

YAK1 protein - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein J1805; protein YOR067c

C:Species: Saccharomyces cerevisiae

C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C/Accession: S57086; S71689

R:Manus, V.; Huang, M.E.; Galibert, F.

submitted to the Protein Sequence Database, September 1995

A/Reference number: S57085

A/Accession: S57086

A/Molecule type: DNA

A/Residues: 1-141 <MAN>

A/Cross-references: UNIPROT:P47118; EMBL:Z49567; NID:91015744; PID:91015745; MIPS:YOR06

R:Huang, M.E.; Manus, V.; Chuat, J.C.; Galibert, F.

Yeast 12, 869-875, 1996

A>Title: Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frame

A/Reference number: S71676; MUID:96437976; PMID:8840504

A/Accession: S71689

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

A/Genes: SGD:YAK1

A/Cross-references: SGD:S0003828; MIPS:YOR067c

A/Map position: 10R

Query Match 2.2%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGL 7
|||||
Db 69 MGILLGL 75

RESULT 66
T45630
hypothetical protein F13G24.250 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T45630
R/Revant, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, December 1999
A/Accession: T45630
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-158 <REV>
A/Cross-references: UNIPROT:Q9SDJ9; EMBL:AL133421
A/Experimental source: cultivar Columbia; BAC clone F13G24
C/Genetics:
A/Map position: 5
A/Introns: 33/3
A/Note: F13G24.250

Query Match 2.2%; Score 7; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LGILLLG 11
|||||
Db 106 LGILLLG 112

RESULT 67
D95096
hemolysin-related protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: D95096
R/Retelid, H.; Nelson, K.R.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; PMID:21357209; PMID:11463916
A/Accession: D95096
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-170 <KUR>
A/Cross-references: UNIPROT:Q97R11; GB:AE005672; PIDN:AAK74965.1; PID:G14972307; GSPDB:C
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP0834

Query Match 2.2%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DGNQVVR 127
|||||
Db 87 DGNQVVR 93

RESULT 68
A97964
conserved hypothetical protein, truncation spr0737 [imported] - Streptococcus pneumoniae
C/Species: Streptococcus pneumoniae

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: A97964
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; Dehoff, B.S.;
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; PMID:21429245; PMID:11544234
A/Accession: A97964
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-170 <KUR>
A/Cross-references: UNIPROT:Q9DQC9; GB:AE007317; PIDN:AAK9541.1; PID:G15458330; GSPDB:C
C/Genetics:
A/Gene: spr0737

Query Match 2.2%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DGNQVVR 127
|||||
Db 87 DGNQVVR 93

RESULT 69
I53285
glucocorticoid-regulated endocrine protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I53285
R/Bloomquist, B.T.; Darlington, D.N.; Mueller, G.P.; Mains, R.E.; Eipper, B.A.
Endocrinology 135, 2714-2722, 1994
A/Title: Regulated endocrine-specific protein-18: a short-lived novel glucocorticoid-re
A/Reference number: I53285; PMID:95080145; PMID:798462
A/Accession: I53285
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-175 <RES>
A/Cross-references: UNIPROT:P47939; GB:U34214; NID:G609540; PIDN:AAA67425.1; PID:G609541
C/Genetics:
A/Gene: RESP18

Query Match 2.2%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 GQVGSQ 221
|||||
Db 39 GQVGSQ 45

RESULT 70
A53523
endocrine secretory protein RESP18 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: A53523
R/Bloomquist, B.T.; Darlington, D.N.; Mains, R.E.; Eipper, B.A.
J. Biol. Chem. 269, 9113-9122, 1994
A/Title: RESP18, a novel endocrine secretory protein transcript, and four other transcr
A/Reference number: A53523; PMID:94179330; PMID:8132649
A/Accession: A53523
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-175 <BLO>
A/Cross-references: UNIPROT:P47940; GB:U25633; NID:G468923; PIDN:AAB59694.1; PID:G46892
C/Keywords: endoplasmic reticulum; polymorphism

Query Match 2.2%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 GQVSEQ 221
 |||||
 Db 39 GQVSEQ 45

RESULT 71

AI0676
 probable exported protein STY1533 [imported] - Salmonella enterica subsp. enterica serov
 C/Species: Salmonella enterica subsp. enterica serovar Typh
 A/Note: this species has also been called Salmonella typhi
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: AI0676
 R/Perkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 ch, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A/Reference number: AB0502; MUID:21534947; PMID:11677608
 A/Accession: AI0676
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-180 <PAR>
 A/Cross-references: GB:AL513382; PTDN:CAD01786.1; PTD:gl6502631; GSPDB:GN00176
 C/Genetic8:
 A/Gene: STY1533

Query Match 2.2%; Score 7; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 ATSTVKQ 259
 |||||
 Db 39 ATSTVKQ 45

RESULT 72

Flagellin A1 precursor [imported] - Halobacterium sp. NRC-1
 H84273
 C/Species: Halobacterium sp. NRC-1
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: H84273
 R/Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
 ; Leitchauer, B.; Keller, K.; Cruz, R.; Danson, M.W.; Hough, D.W.; Maddocks, D.G.; Jabilc
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A/Title: Genome sequence of Halobacterium species NRC-1.
 A/Reference number: A84160; MUID:20504483; PMID:11016950
 A/Accession: H84273
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-207 <STO>
 A/Cross-references: UNIRROT:Q9HQF9; GB:AE004437; NTD:gl0580714; PTDN:AMG19556.1; GSPDB:C
 C/Genetic8:
 A/Gene: FlaA1b
 C/Superfamily: archaeal flagellin

Query Match 2.2%; Score 7; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 VPESVTG 31
 |||||
 Db 195 VPESVTG 201

RESULT 73

IG kappa chain precursor V-J-C regions - rabbit (fragment)
 A/Accession: J02069
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000

C/Accession: A20969; A25448
 R/McCartney-Francis, N.; Skurja Jr., R.M.; Mage, R.G.; Bernslein, K.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 1794-1798, 1984
 A/Title: Kappa-chain allotypes and isotypes in the rabbit: cDNA sequences of clones enc
 otype expression.
 A/Reference number: A20969; MUID:84170388; PMID:6424124

A/Accession: A20969
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-229 <MCC>
 A/Cross-references: GB:U01359; NID:gl65373; PTDN:AAA31334.1; PTD:gl65374
 R/Akmenko, M.A.; Mariane, B.; Rougeon, F.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5180-5183, 1986
 A/Title: Evolution of the immunoglobulin kappa light chain locus in the rabbit: evidenc
 A/Reference number: A94110; MUID:86259753; PMID:3088570
 A/Contents: Ig kappa-1 chain, 69 allotype, J-K1.2 segment
 A/Accession: A25448
 A/Molecule type: DNA
 A/Residues: 111-123 <AKT>
 A/Cross-references: GB:M14067; GB:M14062; GB:M14063; GB:M14064; GB:M14065; GB:M14066; N
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/143-212/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LLAGLLLL 10
 |||||
 Db 1 LLAGLLLL 7

RESULT 74

IG kappa chain - sheep
 S33161
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 C/Accession: S33161
 R/Foley, R.C.; Beh, K.J.
 submitted to the EMBL Data Library, July 1990
 A/Description: Isolation and characterisation of sheep kappa light chain cDNA.
 A/Reference number: S33161
 A/Accession: S33161
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-230 <FOL>
 A/Cross-references: EMBL:X54110; NID:G297103; PTDN:CAA38046.1; PTD:gl364221
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/143-212/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 7; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LLAGLLLL 10
 |||||
 Db 2 LLAGLLLL 8

RESULT 75

FC gamma (IgG) receptor III-B precursor (neutrophil) - human
 J00284
 N/Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gr
 C/Species: Homo sapiens (man)
 C/Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: J00284; S00758; J37628; B32933; A31460
 R/Ravetch, J.V.; Perussia, B.
 J. Exp. Med. 170, 481-497, 1989
 A/Title: Alternative membrane forms of Fc gamma RIII (CD16) on human natural killer cell
 A/Reference number: J10107; MUID:89328325; PMID:2526846
 A/Accession: J00284

A:Molecule type: mRNA
A:Residues: 1-201,'SF',204-233 <PAV>
A:Cross-references: UNIPROT:O75015; GB:J04162
A>Note: the sequence of the receptor from human NK cells, reported in the same paper, differs by 1 end
R:Simmons, D.; Seed, B.
Nature 333, 568-570, 1998
A:title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane protein
A:Reference number: S00758; MUID:88232937; PMID:267436
A:Accession: S00758
A:Molecule type: mRNA
A:Residues: 1-233 <SIM>
A:Cross-references: EMBL:X07934; NID:G29744; PIDN:CAA30758.1; PID:G29745
R:Gesener, J.E.; Grusenmeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A:title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A:Reference number: A55439; MUID:9518131; PMID:7836402
A:Accession: I37628
A:Molecule type: DNA
A:Residues: 1-72 <RRS>
A:Cross-references: EMBL:Z46223; NID:G559446; PIDN:CAA86296.1; PID:G871306
R:Scallion, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeles, J.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A:title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phos
A:Reference number: A32933; MUID:8926947; PMID:2525780
A:Accession: B32933
A:Molecule type: mRNA
A:Residues: 1-121,'E',123-150,'S',152-233 <SCA>
A:Cross-references: GB:M24854; NID:G184851; PIDN:AA53507.1; PID:G306930
R:Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A:title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal
A:Reference number: A31460; MUID:89128838; PMID:2521732
A:Accession: A31460
A:Molecule type: mRNA
A:Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>
A:Cross-references: GB:J04162; NID:G183036; PIDN:AA35881.1; PID:G183037
C:Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the
1, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod
C:Genetics:
A:Gene: GDB:FCGR3B; FCGR3; FCGR3
A:Cross-references: GDB:128176; OMIM:146740
A:Map position: 1q23-1q23
A:Introns: 14/1; 21/1
A>Note: the list of introns is incomplete
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-203/Product: Fc gamma (IgG) receptor IIR-B #status predicted <MAT>
F:40-91/Domain: immunoglobulin homology <IMM1>
F:111-174/Domain: immunoglobulin homology <IMM2>
F:56,63,82,92,180,187/Binding site: carboxylate (Asn) (covalent) #status predicted
F:203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 2.2%; Score 7; DB 1; Length 233;
Best local similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 DSGSYFC 211
DB 166 DSGSYFC 172

Search completed: January 4, 2005, 07:00:38
Job time: 30 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 06:07:15 ; Search time 27 Seconds

(without alignments)
788,447 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 1688
Sequence: 1 MGILLGLLGLHITVDYGR.....AYIMLCRKTSQEHVYEAAR 321

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCURS.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1688	100.0	321	4	US-09-254-465A-2
2	1137	67.4	306	4	US-09-369-247-63
3	178.5	10.6	299	3	US-09-188-930-189
4	178.5	10.6	299	3	US-09-188-930-331
5	178.5	10.6	299	3	US-09-462-270-2
6	178.5	10.6	299	3	US-09-254-465A-1
7	178.5	10.6	299	4	US-09-312-283C-189
8	178.5	10.6	299	4	US-09-312-283C-331
9	178.5	10.6	299	4	US-09-907-794A-119
10	178.5	10.6	299	4	US-09-905-125A-119
11	178.5	10.6	299	4	US-09-902-775A-119
12	178.5	10.6	299	4	US-09-397-243D-3
13	178.5	10.6	299	4	US-09-906-700-119
14	178.5	10.6	299	4	US-10-140-002-166
15	178.5	10.6	299	4	US-09-903-603A-119
16	177	10.5	319	1	US-08-597-495B-22
17	177	10.5	319	3	US-08-068-051A-22
18	177	10.5	319	4	US-09-336-536-67
19	177	10.5	319	4	US-09-254-465A-6
20	176	10.4	270	4	US-09-254-465A-24
21	176	10.4	273	4	US-09-254-465A-26
22	172.5	10.2	316	4	US-09-397-243D-13
23	169.5	10.0	260	4	US-09-254-465A-23
24	169.5	10.0	263	4	US-09-254-465A-25
25	167	9.9	300	4	US-09-254-465A-10
26	167	9.9	300	4	US-09-397-243D-12
27	166	9.8	365	4	US-09-899-634C-4

28	163.5	9.7	261	4	US-09-899-634C-2	Sequence 2, Appl
29	161.5	9.6	318	3	US-09-068-051A-32	Sequence 32, Appl
30	158	9.4	365	2	US-08-979-424-3	Sequence 2, Appl
31	158	9.4	355	3	US-08-928-383B-2	Sequence 2, Appl
32	158	9.4	365	3	US-09-272-496-2	Sequence 2, Appl
33	153.5	9.1	373	4	US-10-140-002-388	Sequence 388, App
34	151	8.9	466	4	US-09-604-107A-8	Sequence 8, Appl
35	142.5	8.4	398	4	US-09-778-510-4	Sequence 4, Appl
36	141.5	8.4	1395	3	US-09-540-245A-15	Sequence 15, Appl
37	140.5	8.3	365	3	US-08-928-383B-23	Sequence 23, Appl
38	140.5	8.3	365	3	US-08-928-383B-24	Sequence 24, Appl
39	140.5	8.3	365	3	US-08-928-383B-26	Sequence 26, Appl
40	138.5	8.2	310	4	US-09-907-794A-423	Sequence 423, App
41	138.5	8.2	310	4	US-09-905-125A-423	Sequence 423, App
42	138.5	8.2	310	4	US-09-902-775A-423	Sequence 423, App
43	138.5	8.2	310	4	US-09-906-700-423	Sequence 423, App
44	138.5	8.2	310	4	US-10-140-002-538	Sequence 538, App
45	138.5	8.2	310	4	US-09-903-603A-423	Sequence 423, App
46	138	8.2	360	4	US-09-907-794A-213	Sequence 213, App
47	138	8.2	360	4	US-09-905-125A-213	Sequence 213, App
48	138	8.2	360	4	US-09-902-775A-213	Sequence 213, App
49	138	8.2	360	4	US-09-906-700-213	Sequence 213, App
50	138	8.2	360	4	US-09-903-603A-213	Sequence 213, App
51	136	8.1	205	3	US-09-462-270-4	Sequence 42, Appl
52	135	8.0	249	4	US-09-336-536-42	Sequence 42, Appl
53	135	8.0	394	4	US-09-336-536-39	Sequence 39, Appl
54	134.5	8.0	153	4	US-09-397-243D-4	Sequence 4, Appl
55	134.5	8.0	450	4	US-09-907-794A-320	Sequence 320, App
56	134.5	8.0	450	4	US-09-905-125A-320	Sequence 320, App
57	134.5	8.0	450	4	US-09-902-775A-320	Sequence 320, App
58	134.5	8.0	450	4	US-09-906-700-320	Sequence 320, App
59	134.5	8.0	450	4	US-10-140-002-378	Sequence 378, App
60	134.5	8.0	450	4	US-09-903-603A-378	Sequence 378, App
61	134	7.9	440	3	US-08-759-628-4	Sequence 4, Appl
62	133.5	7.9	398	4	US-09-778-510-6	Sequence 4, Appl
63	133.5	7.9	398	4	US-09-907-794A-84	Sequence 84, Appl
64	133.5	7.9	398	4	US-09-905-125A-84	Sequence 84, Appl
65	133.5	7.9	398	4	US-09-902-775A-84	Sequence 84, Appl
66	133.5	7.9	398	4	US-09-906-700-84	Sequence 84, Appl
67	133.5	7.9	398	4	US-10-140-002-348	Sequence 348, Appl
68	133.5	7.9	398	4	US-09-903-603A-84	Sequence 84, Appl
69	133.5	7.9	432	4	US-09-778-510-2	Sequence 2, Appl
70	133	7.9	561	4	US-09-866-510-24	Sequence 24, Appl
71	133	7.9	1059	4	US-09-907-794A-290	Sequence 290, App
72	133	7.9	1059	4	US-09-905-125A-290	Sequence 290, App
73	133	7.9	1059	4	US-09-902-775A-290	Sequence 290, App
74	133	7.9	1059	4	US-09-906-700-290	Sequence 290, App
75	133	7.9	1059	4	US-09-903-603A-290	Sequence 290, App
76	133	7.9	1059	4	US-09-866-510-14	Sequence 14, Appl
77	133	7.9	1106	1	US-08-180-195-2	Sequence 2, Appl
78	133	7.9	1106	1	US-08-168-917-2	Sequence 2, Appl
79	133	7.9	1106	1	US-08-477-329-2	Sequence 2, Appl
80	133	7.9	1106	2	US-08-475-458-2	Sequence 2, Appl
81	133	7.9	1106	2	US-08-460-510-2	Sequence 2, Appl
82	133	7.9	1106	2	US-08-460-490-2	Sequence 2, Appl
83	133	7.9	1106	3	US-08-980-400-2	Sequence 2, Appl
84	133	7.9	1106	3	US-08-462-728-4	Sequence 4, Appl
85	133	7.9	1106	3	US-09-583-459A-2	Sequence 2, Appl
86	133	7.9	1106	3	US-09-583-459A-10	Sequence 2, Appl
87	133	7.9	1106	3	US-09-583-449A-2	Sequence 2, Appl
88	133	7.9	1106	3	US-09-435-059-2	Sequence 2, Appl
89	133	7.9	1106	3	US-08-461-917-4	Sequence 4, Appl
90	133	7.9	1106	4	US-08-464-917-4	Sequence 4, Appl
91	133	7.9	1106	4	US-08-464-917-4	Sequence 4, Appl
92	133	7.9	1106	4	US-09-866-510-16	Sequence 16, Appl
93	133	7.9	1106	4	US-09-866-510-18	Sequence 18, Appl
94	133	7.9	1106	4	US-09-866-510-22	Sequence 22, Appl
95	133	7.9	1106	4	US-09-866-510-22	Sequence 22, Appl
96	133	7.9	1106	5	PCT-US92-00730-2	Sequence 2, Appl
97	133	7.9	1106	5	PCT-US92-00862-2	Sequence 2, Appl
98	133	7.9	1119	4	US-09-907-794A-294	Sequence 294, App
99	133	7.9	1119	4	US-09-905-125A-294	Sequence 294, App
100	133	7.9	1119	4	US-09-902-775A-294	Sequence 294, App

101	133	7.9	1119	4	US-09-906-700-294	Sequence 294, App	174	117	6.9	1447	5	PCT-US94-05277-2	Sequence 2, App1
102	133	7.9	1119	4	US-10-140-002-352	Sequence 352, App	175	117	6.9	1745	5	US-09-800-729-89	Sequence 89, App1
103	133	7.9	1119	4	US-09-903-603A-294	Sequence 294, App	176	116.5	6.9	315	2	US-08-414-657D-47	Sequence 47, App1
104	132.5	7.8	630	2	US-08-752-307B-14	Sequence 14, App1	177	116.5	6.9	338	2	US-08-414-657D-42	Sequence 42, App1
105	132.5	7.8	630	3	US-09-707-802-14	Sequence 14, App1	178	116.5	6.9	338	2	US-08-414-657D-43	Sequence 43, App1
106	132.5	7.8	630	3	US-09-991-326-14	Sequence 14, App1	179	116.5	6.9	338	4	US-09-135-080-4	Sequence 4, App1
107	127	7.5	227	4	US-09-205-258-947	Sequence 947, App	180	116.5	6.9	607	2	US-08-752-307B-12	Sequence 12, App1
108	127	7.5	462	2	US-08-752-307B-7	Sequence 7, App1	181	116.5	6.9	607	3	US-09-707-802-11	Sequence 12, App1
109	127	7.5	462	3	US-09-707-802-7	Sequence 7, App1	182	116.5	6.9	607	3	US-09-991-326-12	Sequence 12, App1
110	127	7.5	462	3	US-09-991-326-7	Sequence 7, App1	183	116.5	6.8	303	4	US-09-651-200-23	Sequence 23, App1
111	127	7.5	465	2	US-08-752-307B-5	Sequence 5, App1	184	115.5	6.8	303	4	US-09-441-411-15	Sequence 15, App1
112	127	7.5	465	3	US-09-707-802-5	Sequence 5, App1	185	115.5	6.8	303	4	US-09-441-411-20	Sequence 20, App1
113	127	7.5	465	3	US-09-991-326-5	Sequence 5, App1	186	115.5	6.8	309	2	US-08-456-104-4	Sequence 4, App1
114	126.5	7.5	924	1	US-08-481-130A-28	Sequence 28, App1	187	115.5	6.8	309	3	US-08-479-744B-23	Sequence 23, App1
115	126.5	7.5	924	1	US-08-656-984A-28	Sequence 28, App1	188	115.5	6.8	309	3	US-08-750-757B-23	Sequence 23, App1
116	126.5	7.5	924	1	US-08-485-604-28	Sequence 28, App1	189	115.5	6.8	309	3	US-08-205-697A-21	Sequence 21, App1
117	126.5	7.5	924	1	US-08-487-595-28	Sequence 28, App1	190	115.5	6.8	309	3	US-08-702-525-21	Sequence 21, App1
118	124.5	7.4	387	2	US-09-175-928-2	Sequence 2, App1	191	115.5	6.8	309	4	US-09-651-200-22	Sequence 22, App1
119	123	7.3	313	4	US-09-700-397-4	Sequence 4, App1	192	115.5	6.8	309	4	US-09-667-135-33	Sequence 33, App1
120	123	7.3	344	4	US-09-700-397-3	Sequence 3, App1	193	115.5	6.8	309	4	US-09-425-762-23	Sequence 23, App1
121	123	7.3	344	4	US-10-140-002-376	Sequence 376, App	194	115.5	6.8	309	4	US-09-837-867A-21	Sequence 21, App1
122	122.5	7.3	612	2	US-08-752-307B-11	Sequence 11, App1	195	115.5	6.8	309	4	US-09-206-132-4	Sequence 4, App1
123	122.5	7.3	612	3	US-09-707-802-11	Sequence 11, App1	196	115.5	6.8	309	4	US-09-441-411-13	Sequence 13, App1
124	122.5	7.3	612	3	US-09-991-326-11	Sequence 11, App1	197	115.5	6.8	309	4	US-09-441-411-18	Sequence 18, App1
125	122.5	7.3	1268	3	US-08-506-296B-28	Sequence 28, App1	198	115.5	6.8	309	4	US-09-441-411-24	Sequence 24, App1
126	122	7.2	611	2	US-08-752-307B-10	Sequence 10, App1	199	115.5	6.8	309	5	PCT-US95-02576-21	Sequence 21, App1
127	122	7.2	611	2	US-09-707-802-10	Sequence 10, App1	200	115.5	6.8	314	3	US-08-205-697A-13	Sequence 13, App1
128	122	7.2	611	3	US-09-991-326-10	Sequence 10, App1	201	115.5	6.8	314	3	US-08-702-525-13	Sequence 13, App1
129	120.5	7.1	373	4	US-09-823-038A-60	Sequence 60, App1	202	115.5	6.8	314	4	US-09-837-867A-13	Sequence 13, App1
130	120.5	7.1	440	4	US-09-866-028-61	Sequence 61, App1	203	115.5	6.8	314	4	US-09-441-411-14	Sequence 14, App1
131	120.5	7.1	440	4	US-09-944-457-61	Sequence 61, App1	204	115.5	6.8	314	4	US-09-441-411-19	Sequence 19, App1
132	120.5	7.1	442	4	US-09-944-457-61	Sequence 61, App1	205	115.5	6.8	314	5	PCT-US95-02576-13	Sequence 13, App1
133	120.5	7.1	442	4	US-09-930-803-1	Sequence 1, App1	206	115.5	6.8	356	4	US-09-441-411-11	Sequence 11, App1
134	120.5	7.1	529	4	US-09-383-586-31	Sequence 31, App1	207	115.5	6.8	356	4	US-09-441-411-12	Sequence 12, App1
135	120.5	7.1	529	4	US-09-823-038A-31	Sequence 31, App1	208	115.5	6.8	356	4	US-09-441-411-16	Sequence 16, App1
136	120	7.1	312	4	US-09-254-465A-9	Sequence 9, App1	209	115.5	6.8	356	4	US-09-441-411-17	Sequence 17, App1
137	120	7.1	312	4	US-09-907-794A-64	Sequence 64, App1	210	115.5	6.8	423	4	US-09-778-510-22	Sequence 22, App1
138	120	7.1	312	4	US-09-905-125A-64	Sequence 64, App1	211	115.5	6.8	738	3	US-08-478-208-32	Sequence 32, App1
139	120	7.1	312	4	US-09-902-775A-64	Sequence 64, App1	212	115.5	6.8	738	4	US-09-336-536-73	Sequence 73, App1
140	120	7.1	312	4	US-09-906-770A-64	Sequence 64, App1	213	115.5	6.8	1253	3	US-08-506-296B-14	Sequence 14, App1
141	120	7.1	312	4	US-10-140-002-336	Sequence 336, App	214	115	6.8	315	4	US-09-910-174B-28	Sequence 28, App1
142	120	7.1	312	4	US-09-903-603A-64	Sequence 64, App1	215	115	6.8	315	4	US-09-620-461-28	Sequence 28, App1
143	120	7.1	1101	3	US-08-986-485-2	Sequence 2, App1	216	115	6.8	1209	3	US-09-130-158A-2	Sequence 2, App1
144	119.5	7.1	298	4	US-09-152-060-76	Sequence 76, App1	217	114.5	6.8	431	3	US-09-038-832-4	Sequence 4, App1
145	119.5	7.1	464	2	US-08-602-725-32	Sequence 32, App1	218	114.5	6.8	431	3	US-09-038-832-4	Sequence 4, App1
146	119.5	7.1	467	4	US-09-046-736-2	Sequence 40, App1	219	114.5	6.8	479	4	US-09-723-368-2	Sequence 2, App1
147	119	7.0	365	4	US-09-336-536-40	Sequence 40, App1	220	113.5	6.7	624	4	US-08-467-602-326	Sequence 326, App
148	119	7.0	1091	3	US-08-986-485-5	Sequence 5, App1	221	113.5	6.7	624	4	US-08-411-295F-252	Sequence 252, App
149	118.5	7.0	321	6	5169835-17	Patent No. 5169835	222	113.5	6.7	658	4	US-08-467-602-368	Sequence 368, App
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152	118	7.0	547	2	US-08-473-981A-6	Sequence 6, App1	225	113.5	6.7	841	4	US-08-411-295F-253	Sequence 253, App
153	118	7.0	547	2	US-08-474-087-6	Sequence 6, App1	226	113.5	6.7	875	4	US-08-467-602-369	Sequence 369, App
154	118	7.0	758	2	US-08-874-678-1	Sequence 1, App1	227	113.5	6.7	875	4	US-08-411-295F-295	Sequence 295, App
155	118	7.0	758	3	US-08-643-839-1	Sequence 1, App1	228	113.5	6.7	888	4	US-08-467-602-325	Sequence 325, App
156	118	7.0	758	3	US-09-051-363-24	Sequence 24, App1	229	113.5	6.7	888	4	US-08-411-295F-251	Sequence 251, App
157	118	7.0	758	3	US-09-348-886-14	Sequence 14, App1	230	113.5	6.7	922	4	US-08-467-602-367	Sequence 367, App
158	118	7.0	780	1	US-08-332-538-14	Sequence 14, App1	231	113.5	6.7	922	4	US-08-411-295F-293	Sequence 293, App
159	118	7.0	780	2	US-08-786-164-14	Sequence 14, App1	232	113	6.7	287	2	US-08-414-657D-48	Sequence 48, App1
160	118	7.0	1338	3	US-08-750-0141A-3	Sequence 3, App1	233	113	6.7	304	6	5260223-1	Patent No. 5260223
161	118	7.0	1338	3	US-09-119-014D-6	Sequence 6, App1	234	113	6.7	304	6	US-08-414-657D-44	Sequence 44, App1
162	117.5	7.0	308	2	US-08-414-657D-46	Sequence 46, App1	235	113	6.7	497	4	US-09-499-846-6	Sequence 6, App1
163	117.5	7.0	335	2	US-08-414-657D-2	Sequence 2, App1	236	113	6.7	497	4	US-09-499-846-10	Sequence 10, App1
164	117.5	7.0	335	2	US-08-414-657D-41	Sequence 41, App1	237	112.5	6.7	517	4	US-09-723-368-4	Sequence 4, App1
165	117.5	7.0	338	2	US-09-135-080-2	Sequence 2, App1	238	112	6.6	287	2	US-08-414-657D-49	Sequence 49, App1
166	117.5	7.0	338	4	US-08-414-657D-60	Sequence 60, App1	239	112	6.6	310	2	US-08-414-657D-45	Sequence 45, App1
167	117.5	7.0	338	4	US-09-135-080-8	Sequence 8, App1	240	112	6.6	322	3	US-09-383-586-33	Sequence 33, App1
168	117.5	7.0	338	4	US-09-976-594-404	Sequence 404, App	241	112	6.6	322	4	US-09-823-038A-33	Sequence 33, App1
169	117.5	7.0	615	2	US-08-752-307B-9	Sequence 9, App1	242	112	6.6	613	3	US-08-470-335-230	Sequence 230, App
170	117.5	7.0	615	3	US-09-707-802-9	Sequence 9, App1	243	112	6.6	613	4	US-08-467-602-329	Sequence 329, App
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172	117	6.9	292	4	US-09-800-729-175	Sequence 175, App	245	112	6.6	633	4	US-08-467-602-335	Sequence 335, App
173	117	6.9	1447	3	US-09-041-886-25	Sequence 25, App1	246	112	6.6	633	4	US-08-411-295F-261	Sequence 261, App

247	112	6	6	647	4	US-08-467-602-371	Sequence 371, App	320	108	6	4	444	3	US-08-660-531-5	Sequence 5, Appl
248	112	6	6	647	4	US-08-411-295F-297	Sequence 297, App	321	108	6	4	868	1	US-08-374-834-1	Sequence 1, Appl
249	112	6	6	667	4	US-08-467-602-377	Sequence 377, App	322	108	6	4	868	2	US-08-644-271-1	Sequence 1, Appl
250	112	6	6	667	4	US-08-411-295F-303	Sequence 303, App	323	108	6	4	868	4	US-09-077-955-1	Sequence 1, Appl
251	112	6	6	830	3	US-08-470-335-231	Sequence 231, App	324	107.5	6	4	290	4	US-09-910-174B-19	Sequence 19, Appl
252	112	6	6	830	4	US-08-467-602-330	Sequence 330, App	325	107.5	6	4	290	4	US-09-620-461-1	Sequence 19, Appl
253	112	6	6	830	4	US-08-411-295F-256	Sequence 256, App	326	107.5	6	4	340	4	US-09-651-200-2	Sequence 2, Appl
254	112	6	6	830	4	US-08-467-602-336	Sequence 336, App	327	107.5	6	4	330	4	US-09-651-200-25	Sequence 25, Appl
255	112	6	6	850	4	US-08-411-295F-262	Sequence 262, App	328	107.5	6	4	330	4	US-09-910-174B-17	Sequence 17, Appl
256	112	6	6	850	4	US-08-467-602-372	Sequence 372, App	329	107.5	6	4	330	4	US-09-620-461-1	Sequence 17, Appl
257	112	6	6	864	4	US-08-411-295F-298	Sequence 298, App	330	107.5	6	4	441	4	US-09-651-200-4	Sequence 4, Appl
258	112	6	6	877	3	US-08-470-335-232	Sequence 232, App	331	107.5	6	4	1297	3	US-09-540-245A-17	Sequence 17, Appl
259	112	6	6	877	4	US-08-467-602-331	Sequence 331, App	332	107.5	6	4	1311	1	US-08-340-031-5	Sequence 5, Appl
260	112	6	6	877	4	US-08-411-295F-257	Sequence 257, App	333	107.5	6	4	1311	3	US-08-901-710-5	Sequence 5, Appl
261	112	6	6	884	4	US-08-467-602-378	Sequence 378, App	334	107	6	3	332	4	US-10-140-002-386	Sequence 386, App
262	112	6	6	884	4	US-08-411-295F-304	Sequence 304, App	335	107	6	3	624	2	US-08-642-406A-22	Sequence 22, App
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264	112	6	6	897	4	US-08-467-602-337	Sequence 337, App	337	107	6	3	624	4	US-09-199-534-22	Sequence 22, App
265	112	6	6	911	4	US-08-411-295F-263	Sequence 263, App	338	107	6	3	733	3	US-08-434-000A-2	Sequence 2, Appl
266	112	6	6	911	4	US-08-467-602-373	Sequence 373, App	339	107	6	3	733	3	US-09-312-157-2	Sequence 2, Appl
267	112	6	6	911	4	US-08-411-295F-299	Sequence 299, App	340	106.5	6	3	731	1	US-07-921-807B-5	Sequence 5, Appl
268	112	6	6	931	4	US-08-467-602-379	Sequence 379, App	341	106.5	6	3	731	1	US-08-441-944A-5	Sequence 5, Appl
269	112	6	6	946	5	PCT-US95-08493-13	Sequence 13, App	342	106.5	6	3	731	3	US-08-439-992A-3	Sequence 3, Appl
270	111.5	6	6	344	2	US-08-602-725-34	Sequence 34, App	343	106	6	3	729	1	US-07-640-029-3	Sequence 4, Appl
271	111	6	6	252	2	US-08-414-657D-56	Sequence 56, App	344	106	6	3	1474	4	US-09-677-046A-4	Sequence 4, Appl
272	111	6	6	252	2	US-08-414-657D-57	Sequence 57, App	345	106	6	3	1953	1	US-09-917-254-92	Sequence 92, Appl
273	110.5	6	5	349	4	US-09-924-103-4	Sequence 57, App	346	105.5	6	2	246	1	US-07-843-125-11	Sequence 11, Appl
274	110.5	6	5	330	2	US-08-979-424-1	Sequence 4, Appl	347	105.5	6	2	331	5	PCT-US93-05703-2	Sequence 2, Appl
275	110.5	6	5	330	4	US-09-907-794A-39	Sequence 39, App	348	105.5	6	2	408	3	US-09-724-864-62	Sequence 62, App
276	110.5	6	5	330	4	US-09-905-125A-39	Sequence 39, App	349	105.5	6	2	589	2	US-08-724-394A-1	Sequence 1, Appl
277	110.5	6	5	330	4	US-09-902-775A-39	Sequence 39, App	350	105.5	6	2	604	3	US-08-470-335-227	Sequence 27, App
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279	110.5	6	5	330	4	US-10-140-002-338	Sequence 38, App	352	105.5	6	2	604	4	US-08-411-295F-244	Sequence 244, App
280	110.5	6	5	330	4	US-09-903-603A-39	Sequence 39, App	353	105.5	6	2	638	4	US-08-467-602-360	Sequence 360, App
281	110.5	6	5	513	4	US-09-910-174B-18	Sequence 18, App	354	105.5	6	2	628	4	US-08-411-295F-286	Sequence 286, App
282	110.5	6	5	513	4	US-09-620-461-18	Sequence 18, App	355	105.5	6	2	651	1	US-09-270-767-44877	Sequence 44877, A
283	110.5	6	5	518	4	US-09-919-172-30	Sequence 20, App	356	105.5	6	2	733	1	US-07-640-029-4	Sequence 4, Appl
284	110.5	6	5	1070	4	US-09-961-403-3	Sequence 3, Appl	357	105.5	6	2	733	1	US-07-921-807B-6	Sequence 6, Appl
285	110	6	5	316	4	US-09-910-174B-24	Sequence 24, App	358	105.5	6	2	733	1	US-08-441-944A-6	Sequence 6, Appl
286	110	6	5	316	4	US-09-620-461-24	Sequence 24, App	359	105.5	6	2	733	3	US-08-439-992A-4	Sequence 4, Appl
287	110	6	5	547	1	US-08-314-615-1	Sequence 1, Appl	360	105.5	6	2	817	1	US-07-640-029-2	Sequence 2, Appl
288	110	6	5	547	1	US-08-314-362-1	Sequence 1, Appl	361	105.5	6	2	820	1	US-07-921-807B-3	Sequence 3, Appl
289	110	6	5	547	1	US-08-433-010-1	Sequence 1, Appl	362	105.5	6	2	820	1	US-08-441-944A-3	Sequence 3, Appl
290	110	6	5	547	1	US-08-482-882-1	Sequence 1, Appl	363	105.5	6	2	820	3	US-08-439-992A-1	Sequence 1, Appl
291	110	6	5	547	2	US-08-483-389-1	Sequence 1, Appl	364	105.5	6	2	821	3	US-08-470-335-228	Sequence 28, App
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294	110	6	5	547	2	US-08-483-932-1	Sequence 1, Appl	367	105.5	6	2	822	1	US-07-921-807B-4	Sequence 1, Appl
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296	110	6	5	547	3	US-08-714-017-1	Sequence 1, Appl	369	105.5	6	2	822	1	US-08-459-296-2	Sequence 2, Appl
297	110	6	5	547	3	US-08-863-790-1	Sequence 1, Appl	370	105.5	6	2	822	1	US-08-441-944A-4	Sequence 4, Appl
298	110	6	5	547	3	US-08-475-680-1	Sequence 1, Appl	371	105.5	6	2	822	2	US-08-451-822A-12	Sequence 12, App
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313	109	6	5	547	4	US-09-499-846-12	Sequence 12, App	386	105	6	2	828	4	US-08-261-304-2	Sequence 2, Appl
314	109	6	5	547	4	US-09-499-846-12	Sequence 12, App	387	104.5	6	2	1509	4	US-09-677-046A-2	Sequence 412, App
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317	108	6	4	421	3	US-08-659-984A-1	Sequence 1, Appl	390	104	6	2	409	4	US-08-467-602-221	Sequence 221, App
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419	103.5	6.1	534	4	US-09-651-200-24	Sequence 24, App1	492	102	6.0	319	4	US-09-910-174B-12	Sequence 12, App1
420	103.5	6.1	668	1	US-08-232-538-13	Sequence 13, App1	493	102	6.0	319	4	US-09-620-461-12	Sequence 12, App1
421	103.5	6.1	668	2	US-08-786-164-13	Sequence 13, App1	494	102	6.0	347	4	US-09-667-135-4	Sequence 4, App1
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425	103.5	6.1	767	3	US-09-348-886-2	Sequence 2, App1	498	102	6.0	698	2	US-08-602-725-36	Sequence 36, App1
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433	103.5	6.1	1651	3	US-09-540-245A-18	Sequence 18, App1	506	101	6.0	458	3	US-09-517-605-3	Sequence 3, App1
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436	102.5	6.1	326	5	US-08-225-477B-6	Sequence 6, App1	509	101	6.0	890	3	US-08-170-558-2	Sequence 2, App1
437	102.5	6.1	326	5	PCT-US95-04353-6	Sequence 6, App1	510	101	6.0	890	3	US-08-447-314-2	Sequence 2, App1
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439	102.5	6.1	398	4	US-08-411-295F-150	Sequence 150, App	512	101	6.0	911	1	US-08-286-305A-1	Sequence 1, App1
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547	100	5.9	322	4	US-09-620-461-29	Sequence 29, App1	620	97.5	5.8	97	4	US-10-574-978-28	Sequence 28, App1
548	100	5.9	484	4	US-10-092-138A-25	Sequence 25, App1	621	97.5	5.8	246	1	US-08-197-834-7	Sequence 7, App1
549	99.5	5.9	244	4	US-09-244-369B-1	Sequence 1, App1	622	97.5	5.8	342	2	US-08-724-394A-6	Sequence 6, App1
550	99.5	5.9	244	4	US-09-940-391-1	Sequence 1, App1	623	97.5	5.8	344	4	US-08-467-602-245	Sequence 245, App
551	99.5	5.9	536	2	US-08-752-307B-13	Sequence 13, App1	624	97.5	5.8	344	4	US-08-411-295F-171	Sequence 171, App
552	99.5	5.9	536	3	US-09-707-802-13	Sequence 13, App1	625	97.5	5.8	344	4	US-08-467-602-251	Sequence 251, App
553	99.5	5.9	536	3	US-09-991-326-13	Sequence 13, App1	626	97.5	5.8	344	4	US-08-411-295F-177	Sequence 177, App
554	99.5	5.9	610	3	US-08-470-335-836	Sequence 236, App	627	97.5	5.8	581	4	US-08-467-602-246	Sequence 246, App
555	99.5	5.9	610	4	US-08-467-602-332	Sequence 332, App	628	97.5	5.8	581	4	US-08-411-295F-112	Sequence 172, App
556	99.5	5.9	610	4	US-08-411-295F-258	Sequence 258, App	629	97.5	5.8	601	4	US-08-467-602-252	Sequence 252, App
557	99.5	5.9	644	4	US-08-467-602-374	Sequence 374, App	630	97.5	5.8	601	4	US-08-411-295F-178	Sequence 178, App
558	99.5	5.9	644	4	US-08-411-295F-300	Sequence 300, App	631	97.5	5.8	602	1	US-08-168-091A-2	Sequence 2, App1
559	99.5	5.9	827	3	US-08-470-335-237	Sequence 237, App	632	97.5	5.8	628	1	US-08-467-602-247	Sequence 247, App
560	99.5	5.9	827	4	US-08-467-602-333	Sequence 333, App	633	97.5	5.8	628	4	US-08-411-295F-113	Sequence 173, App
561	99.5	5.9	827	4	US-08-411-295F-259	Sequence 259, App	634	97.5	5.8	648	4	US-08-467-602-253	Sequence 253, App
562	99.5	5.9	861	4	US-08-467-602-375	Sequence 375, App	635	97.5	5.8	648	4	US-08-411-295F-179	Sequence 179, App
563	99.5	5.9	861	4	US-08-411-295F-301	Sequence 301, App	636	97.5	5.8	821	1	US-08-339-578-2	Sequence 2, App1
564	99.5	5.9	874	3	US-08-470-335-238	Sequence 238, App	637	97	5.7	340	3	US-09-188-930-184	Sequence 184, App
565	99.5	5.9	874	4	US-08-467-602-334	Sequence 334, App	638	97	5.7	340	4	US-09-312-283C-164	Sequence 164, App
566	99.5	5.9	874	4	US-08-411-295F-260	Sequence 260, App	639	97	5.7	348	2	US-08-284-391B-29	Sequence 29, App1
567	99.5	5.9	908	4	US-08-467-602-376	Sequence 376, App	640	97	5.7	348	3	US-09-218-950-29	Sequence 29, App1
568	99.5	5.9	908	4	US-08-411-295F-302	Sequence 302, App	641	97	5.7	388	4	US-08-394-388A-29	Sequence 29, App1
569	99	5.9	341	4	US-09-336-536-29	Sequence 29, App1	642	97	5.7	402	1	US-08-336-311-1	Sequence 1, App1
570	99	5.9	370	4	US-09-336-536-28	Sequence 28, App1	643	97	5.7	402	3	US-08-457-918-1	Sequence 1, App1
571	99	5.9	374	3	US-09-046-736-4	Sequence 4, App1	644	97	5.7	402	3	US-10-157-408-1	Sequence 1, App1
572	99	5.9	375	4	US-08-467-602-242	Sequence 242, App	645	97	5.7	457	4	US-08-328-500-9	Sequence 9, App1
573	99	5.9	375	4	US-08-411-295F-168	Sequence 168, App	646	97	5.7	458	3	US-08-466-368-4	Sequence 4, App1
574	99	5.9	388	1	US-08-445-640-6	Sequence 6, App1	647	97	5.7	462	2	US-08-417-495-5	Sequence 5, App1
575	99	5.9	388	3	US-08-170-558-6	Sequence 6, App1	648	97	5.7	462	2	US-08-384-391B-5	Sequence 5, App1
576	99	5.9	388	3	US-08-447-314-6	Sequence 6, App1	649	97	5.7	462	3	US-09-218-950-5	Sequence 5, App1
577	99	5.9	388	3	US-08-445-461-6	Sequence 6, App1	650	97	5.7	462	3	US-08-394-388A-5	Sequence 5, App1
578	99	5.9	394	6	5223418-2	Patent No. 5223418	651	97	5.7	462	5	PCT-US92-01785-5	Sequence 5, App1
579	99	5.9	398	4	US-08-467-602-287	Sequence 287, App	652	97	5.7	532	2	PCT-US95-00454-5	Sequence 5, App1
580	99	5.9	398	4	US-08-411-295F-213	Sequence 213, App	653	97	5.7	532	2	US-08-417-495-6	Sequence 6, App1
581	99	5.9	418	4	US-08-467-602-293	Sequence 293, App	654	97	5.7	532	2	US-08-384-391B-6	Sequence 6, App1
582	99	5.9	418	4	US-08-411-295F-219	Sequence 219, App	655	97	5.7	532	3	US-09-218-950-6	Sequence 6, App1
583	99	5.9	458	3	US-09-039-555B-15	Sequence 15, App1	656	97	5.7	532	4	US-08-394-388A-6	Sequence 6, App1
584	99	5.9	584	4	US-09-910-174B-16	Sequence 16, App1	657	97	5.7	532	5	PCT-US92-01785-6	Sequence 6, App1
585	99	5.9	584	4	US-09-620-461-16	Sequence 16, App1	658	97	5.7	532	5	PCT-US95-00454-6	Sequence 6, App1
586	99	5.9	592	4	US-08-467-602-243	Sequence 243, App	659	97	5.7	575	2	US-08-417-495-4	Sequence 4, App1
587	99	5.9	592	4	US-08-411-295F-169	Sequence 169, App	660	97	5.7	575	2	US-08-384-391B-4	Sequence 4, App1
588	99	5.9	615	4	US-08-467-602-288	Sequence 288, App	661	97	5.7	575	3	US-09-218-950-4	Sequence 4, App1
589	99	5.9	615	4	US-08-411-295F-214	Sequence 214, App	662	97	5.7	575	4	US-08-394-388A-4	Sequence 4, App1
590	99	5.9	635	4	US-08-467-602-294	Sequence 294, App	663	97	5.7	575	5	PCT-US92-01785-4	Sequence 4, App1
591	99	5.9	635	4	US-08-411-295F-220	Sequence 220, App	664	97	5.7	575	5	PCT-US95-00454-4	Sequence 4, App1
592	99	5.9	639	4	US-08-467-602-241	Sequence 241, App	665	97	5.7	601	3	US-08-470-335-233	Sequence 233, App
593	99	5.9	639	4	US-08-411-295F-167	Sequence 167, App	666	97	5.7	601	4	US-08-467-602-323	Sequence 233, App
594	99	5.9	662	4	US-08-467-602-289	Sequence 289, App	667	97	5.7	601	4	US-08-411-295F-249	Sequence 249, App
595	99	5.9	662	4	US-08-411-295F-215	Sequence 215, App	668	97	5.7	630	4	US-08-472-888A-6	Sequence 6, App1
596	99	5.9	662	4	US-08-467-602-295	Sequence 295, App	669	97	5.7	635	4	US-08-467-602-365	Sequence 365, App
597	99	5.9	682	4	US-08-411-295F-221	Sequence 221, App	670	97	5.7	635	4	US-08-411-295F-291	Sequence 291, App
598	98.5	5.8	324	4	US-09-910-174B-6	Sequence 6, App1	671	97	5.7	662	1	US-08-261-304-7	Sequence 7, App1
599	98.5	5.8	324	4	US-09-620-461-6	Sequence 6, App1	672	97	5.7	735	5	PCT-US93-00031-13	Sequence 13, App1
600	98.5	5.8	434	2	US-08-487-113D-120	Sequence 120, App	673	97	5.7	736	5	PCT-US93-00031-15	Sequence 15, App1
601	98.5	5.8	434	2	US-08-720-420A-120	Sequence 120, App	674	97	5.7	739	3	US-08-482-073-6	Sequence 6, App1
602	98.5	5.8	602	1	US-08-428-926-5	Sequence 5, App1	675	97	5.7	739	3	PCT-US93-00031-9	Sequence 9, App1
603	98.5	5.8	602	1	US-08-428-927-5	Sequence 5, App1	676	97	5.7	806	2	US-08-443-861-5	Sequence 5, App1
604	98.5	5.8	602	1	US-08-428-928-5	Sequence 5, App1	677	97	5.7	806	3	US-08-193-829B-5	Sequence 5, App1
605	98.5	5.8	602	1	US-08-428-929-5	Sequence 5, App1	678	97	5.7	818	3	US-08-470-335-234	Sequence 234, App
606	98	5.8	602	1	US-08-339-517-5	Sequence 5, App1	679	97	5.7	818	4	US-08-467-602-321	Sequence 321, App
607	98	5.8	240	4	US-09-270-767-321A	Sequence 47351, A	680	97	5.7	818	4	US-08-411-295F-247	Sequence 247, App
608	98	5.8	243	1	US-08-230-843-4	Sequence 4, App1	681	97	5.7	822	4	US-08-467-602-363	Sequence 363, App
609	98	5.8	243	2	US-08-636-936-4	Sequence 4, App1	682	97	5.7	822	4	US-08-411-295F-289	Sequence 289, App
610	98	5.8	246	4	US-09-336-536-31	Sequence 31, App1	683	97	5.7	865	3	US-08-470-335-235	Sequence 235, App
611	98	5.8	295	6	5223394-9	Patent No. 5223394	684	97	5.7	865	4	US-08-467-602-322	Sequence 322, App

685	97	5.7	865	4	US-08-411-295F-248	Sequence 248, App	758	95	5.6	649	4	US-09-269-939A-8	Sequence 8, Appl1
686	97	5.7	899	4	US-08-467-602-364	Sequence 364, App	759	95	5.6	879	1	US-08-554-612C-1	Sequence 1, Appl1
687	97	5.7	899	4	US-08-411-295F-290	Sequence 290, App	760	95	5.6	1801	2	US-08-447-464-3	Sequence 3, Appl1
688	97	5.7	1367	1	US-07-813-593-4	Sequence 4, Appl1	761	95	5.6	1901	2	US-08-716-679-3	Sequence 3, Appl1
689	97	5.7	1367	1	US-07-977-451-6	Sequence 6, Appl1	762	94.5	5.6	194	3	US-08-630-172-14	Sequence 14, Appl1
690	97	5.7	1367	1	US-07-946-507-4	Sequence 6, Appl1	763	94.5	5.6	194	3	US-09-375-418-14	Sequence 14, Appl1
691	97	5.7	1367	1	US-08-252-517-6	Sequence 6, Appl1	764	94.5	5.6	328	3	US-09-560-639-9	Sequence 9, Appl1
692	97	5.7	1367	1	US-07-906-397A-6	Sequence 6, Appl1	765	94.5	5.6	328	3	US-09-173-151A-25	Sequence 25, Appl1
693	97	5.7	1367	1	US-08-601-891-6	Sequence 6, Appl1	766	94.5	5.6	477	2	US-09-032-337-45	Sequence 45, Appl1
694	97	5.7	1367	2	US-08-443-861-2	Sequence 2, Appl1	767	94.5	5.6	477	2	US-08-359-705B-4	Sequence 4, Appl1
695	97	5.7	1367	2	US-09-021-324-6	Sequence 2, Appl1	768	94.5	5.6	477	2	US-08-286-846A-4	Sequence 4, Appl1
696	97	5.7	1367	3	US-08-193-829B-2	Sequence 6, Appl1	769	94.5	5.6	477	2	US-08-457-880A-4	Sequence 4, Appl1
697	97	5.7	1367	4	US-09-872-136B-6	Sequence 6, Appl1	770	94.5	5.6	477	3	US-08-444-622A-4	Sequence 4, Appl1
698	97	5.7	1367	5	PCT-US92-02750-8	Sequence 6, Appl1	771	94.5	5.6	477	3	US-08-942-562-4	Sequence 4, Appl1
699	97	5.7	1367	5	PCT-US92-05401-6	Sequence 6, Appl1	772	94.5	5.6	477	3	US-09-156-923-4	Sequence 4, Appl1
700	97	5.7	1367	5	PCT-US92-09893-6	Sequence 6, Appl1	773	94.5	5.6	556	3	US-09-560-639-8	Sequence 8, Appl1
701	96.5	5.7	158	3	US-09-560-639-13	Sequence 13, Appl1	774	94.5	5.6	610	2	US-08-724-394A-5	Sequence 5, Appl1
702	96.5	5.7	439	3	US-09-383-586-32	Sequence 32, Appl1	775	94.5	5.6	822	2	US-08-359-705B-2	Sequence 2, Appl1
703	96.5	5.7	439	4	US-09-823-038A-32	Sequence 32, Appl1	776	94.5	5.6	822	2	US-08-286-846A-2	Sequence 2, Appl1
704	96.5	5.7	489	4	US-09-667-135-30	Sequence 30, Appl1	777	94.5	5.6	822	3	US-08-457-880A-2	Sequence 2, Appl1
705	96.5	5.7	782	4	US-09-684-708A-21	Sequence 21, Appl1	778	94.5	5.6	822	3	US-08-444-622A-2	Sequence 2, Appl1
706	96.5	5.7	820	1	US-08-166-717D-6	Sequence 6, Appl1	779	94.5	5.6	822	3	US-08-942-562-2	Sequence 2, Appl1
707	96	5.7	389	4	US-08-467-602-213	Sequence 213, App	780	94.5	5.6	822	3	US-09-156-923-2	Sequence 2, Appl1
708	96	5.7	389	4	US-08-411-295F-139	Sequence 139, App	781	94.5	5.6	847	1	US-08-286-302A-5	Sequence 5, Appl1
709	96	5.7	423	4	US-08-467-602-255	Sequence 255, App	782	94.5	5.6	847	2	US-08-441-104A-5	Sequence 5, Appl1
710	96	5.7	423	4	US-08-467-602-255	Sequence 181, App	783	94.5	5.6	847	2	US-08-440-816A-5	Sequence 5, Appl1
711	96	5.7	469	3	US-08-753-007A-8	Sequence 8, Appl1	784	94.5	5.6	847	3	US-09-417-381A-5	Sequence 5, Appl1
712	96	5.7	469	3	US-09-398-496-8	Sequence 8, Appl1	785	94.5	5.6	888	1	US-08-445-640-35	Sequence 35, Appl1
713	96	5.7	469	3	US-08-467-602-214	Sequence 214, App	786	94.5	5.6	888	1	US-08-170-558-35	Sequence 35, Appl1
714	96	5.7	606	4	US-08-411-295F-140	Sequence 140, App	787	94.5	5.6	888	3	US-08-447-314-35	Sequence 35, Appl1
715	96	5.7	606	4	US-07-847-743B-26	Sequence 26, Appl1	788	94.5	5.6	888	3	US-08-445-461-35	Sequence 35, Appl1
716	96	5.7	625	1	US-08-456-201-26	Sequence 26, Appl1	789	94.5	5.6	910	4	US-09-313-942-28	Sequence 28, Appl1
717	96	5.7	625	2	US-08-456-241-26	Sequence 26, Appl1	790	94.5	5.6	999	4	US-08-252-626A-2	Sequence 2, Appl1
718	96	5.7	625	5	PCT-US92-04295A-26	Sequence 26, Appl1	791	94	5.6	198	4	US-09-569-611C-34	Sequence 34, Appl1
719	96	5.7	640	4	US-08-467-602-256	Sequence 256, App	792	94	5.6	203	4	US-09-270-767-603A5	Sequence 603A5, A
720	96	5.7	640	4	US-09-307-794A-292	Sequence 292, App	793	94	5.6	261	4	US-09-270-767-32898	Sequence 32898, A
721	96	5.7	640	4	US-09-905-125A-292	Sequence 292, App	794	94	5.6	261	4	US-09-270-767-48115	Sequence 48115, A
722	96	5.7	640	4	US-09-902-775A-292	Sequence 292, App	795	94	5.6	422	1	US-08-036-555B-170	Sequence 170, App
723	96	5.7	640	4	US-09-906-700-292	Sequence 292, App	796	94	5.6	422	1	US-08-469-565A-170	Sequence 170, App
724	96	5.7	640	4	US-10-140-002-368	Sequence 368, App	797	94	5.6	422	1	US-08-428-926-3	Sequence 3, Appl1
725	96	5.7	640	4	US-08-411-295F-182	Sequence 182, App	798	94	5.6	422	1	US-08-249-322A-170	Sequence 170, App
726	96	5.7	640	4	US-09-903-603A-292	Sequence 292, App	799	94	5.6	422	1	US-08-428-927-3	Sequence 3, Appl1
727	96	5.7	647	3	US-08-753-007A-32	Sequence 32, Appl1	800	94	5.6	422	1	US-08-428-298-3	Sequence 3, Appl1
728	96	5.7	647	3	US-09-398-496-32	Sequence 32, Appl1	801	94	5.6	422	1	US-08-339-517-3	Sequence 3, Appl1
729	96	5.7	650	3	US-09-310-463-2	Sequence 2, Appl1	802	94	5.6	422	1	US-08-469-565A-170	Sequence 170, App
730	96	5.7	650	3	US-08-842-248A-2	Sequence 2, Appl1	803	94	5.6	422	2	US-08-734-591A-170	Sequence 170, App
731	96	5.7	651	3	US-08-985-950-22	Sequence 22, Appl1	804	94	5.6	422	2	US-08-469-660-170	Sequence 170, App
732	96	5.7	651	4	US-09-546-049-22	Sequence 22, Appl1	805	94	5.6	422	3	US-08-341-018-72	Sequence 72, Appl1
733	96	5.7	653	4	US-08-467-602-212	Sequence 212, App	806	94	5.6	422	3	US-08-470-335-170	Sequence 170, App
734	96	5.7	653	4	US-08-411-295F-138	Sequence 138, App	807	94	5.6	422	3	US-08-735-021-170	Sequence 170, App
735	96	5.7	659	1	US-07-847-743B-8	Sequence 8, Appl1	808	94	5.6	422	3	US-08-734-664A-170	Sequence 170, App
736	96	5.7	659	1	US-07-847-743B-13	Sequence 13, Appl1	809	94	5.6	422	3	US-08-470-339-170	Sequence 170, App
737	96	5.7	659	1	US-08-456-201-8	Sequence 8, Appl1	810	94	5.6	422	4	US-08-467-603-170	Sequence 170, App
738	96	5.7	659	1	US-08-456-201-13	Sequence 13, Appl1	811	94	5.6	422	4	US-08-411-295F-65	Sequence 65, Appl1
739	96	5.7	659	2	US-08-330-161-11	Sequence 11, Appl1	812	94	5.6	422	4	US-08-411-295F-66	Sequence 66, Appl1
740	96	5.7	659	2	US-08-456-241-8	Sequence 8, Appl1	813	94	5.6	422	4	US-08-411-295F-69	Sequence 69, Appl1
741	96	5.7	659	2	US-08-456-241-13	Sequence 13, Appl1	814	94	5.6	422	4	US-08-411-295F-103	Sequence 103, Appl1
742	96	5.7	659	2	US-08-440-401-11	Sequence 11, Appl1	815	94	5.6	422	5	PCT-US94-05083C-166	Sequence 166, App
743	96	5.7	659	2	US-08-419-878B-11	Sequence 11, Appl1	816	94	5.6	422	5	PCT-US94-05083C-185	Sequence 185, App
744	96	5.7	659	3	US-09-173-480-11	Sequence 11, Appl1	817	94	5.6	422	5	PCT-US95-06846A-170	Sequence 170, App
745	96	5.7	669	3	PCT-US92-04295A-8	Sequence 8, Appl1	818	94	5.6	458	6	5223394-7	Patent No. 5223394
746	96	5.7	669	5	PCT-US92-04295A-13	Sequence 254, App	819	94	5.6	635	3	US-08-470-335-247	Sequence 247, App
747	96	5.7	687	4	US-08-467-602-254	Sequence 254, App	820	94	5.6	635	4	US-08-467-602-302	Sequence 302, App
748	96	5.7	687	4	US-08-411-295F-180	Sequence 180, App	821	94	5.6	635	4	US-08-411-295F-228	Sequence 228, App
749	96	5.7	1140	4	US-09-579-692B-8	Sequence 8, Appl1	822	94	5.6	637	4	US-09-569-611C-35	Sequence 35, Appl1
750	96	5.7	1638	4	US-09-071-035-258	Sequence 258, App	823	94	5.6	669	4	US-08-467-602-344	Sequence 344, App
751	96	5.7	1638	4	US-09-071-035-262	Sequence 262, App	824	94	5.6	669	4	US-08-411-295F-270	Sequence 270, Appl1
752	96	5.7	1638	4	US-09-071-035-266	Sequence 266, App	825	94	5.6	805	3	US-08-985-526-34	Sequence 34, Appl1
753	96	5.7	1747	4	US-09-134-000C-55999	Sequence 5999, App	826	94	5.6	852	3	US-08-470-335-248	Sequence 248, App
754	95.5	5.7	652	3	US-09-310-463-4	Sequence 4, Appl1	827	94	5.6	852	4	US-08-467-602-300	Sequence 300, App
755	95.5	5.7	652	3	US-08-842-248A-4	Sequence 4, Appl1	828	94	5.6	852	4	US-08-411-295F-326	Sequence 326, App
756	95	5.6	287	3	US-08-862-124-17	Sequence 17, Appl1	829	94	5.6	886	4	US-08-467-602-342	Sequence 342, App
757	95	5.6	649	4	US-09-499-522-14	Sequence 14, Appl1	830	94	5.6	886	4	US-08-411-295F-268	Sequence 268, App

831	94	5.6	899	3	US-08-470-335-249	Sequence 249, App	904	92	5.5	302	4	US-09-549-067A-32	Sequence 32, App1
832	94	5.6	899	4	US-08-467-602-301	Sequence 301, App	905	92	5.5	351	4	US-09-756-983-18	Sequence 18, App1
833	94	5.6	899	4	US-08-411-295F-227	Sequence 227, App	906	92	5.5	411	3	US-08-470-339-189	Sequence 189, App
834	94	5.6	933	4	US-08-467-602-343	Sequence 343, App	907	92	5.5	414	3	US-08-470-339-188	Sequence 188, App
835	94	5.6	933	4	US-08-411-295F-269	Sequence 269, App	908	92	5.5	422	3	US-08-753-007A-9	Sequence 9, App1
836	94	5.6	983	3	US-09-412-554A-2	Sequence 2, App1	909	92	5.5	422	3	US-09-398-496-9	Sequence 9, App1
837	93.5	5.5	143	2	US-08-653-402B-8	Sequence 8, App1	910	92	5.5	422	4	US-08-467-602-224	Sequence 324, App
838	93.5	5.5	259	3	US-09-560-639-11	Sequence 11, App1	911	92	5.5	422	4	US-08-411-295F-225	Sequence 250, App
839	93.5	5.5	296	4	US-09-667-135-36	Sequence 36, App1	912	92	5.5	425	3	US-08-470-335-226	Sequence 226, App
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844	93.5	5.5	329	2	US-08-101-624-2	Sequence 2, App1	917	92	5.5	456	4	US-08-467-602-166	Sequence 166, App
845	93.5	5.5	329	3	US-08-479-744A-2	Sequence 2, App1	918	92	5.5	456	4	US-08-411-295F-229	Sequence 229, App
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878	92.5	5.5	309	4	US-09-404-879A-392	Sequence 392, App	951	91.5	5.4	338	1	US-08-442-043A-17	Sequence 17, App1
879	92.5	5.5	309	4	US-09-667-857-392	Sequence 392, App	952	91.5	5.4	338	4	US-08-441-893A-17	Sequence 17, App1
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883	92.5	5.5	424	6	US-08-336-583-2	Sequence 2, App1	956	91.5	5.4	576	2	US-08-381-603-4	Sequence 4, App1
884	92.5	5.5	426	1	PCT-US95-13795-2	Sequence 2, App1	957	91.5	5.4	576	3	US-08-924-376-4	Sequence 4, App1
885	92.5	5.5	426	1	PCT-US95-13795-2	Sequence 2, App1	958	91.5	5.4	576	3	US-08-685-212-4	Sequence 4, App1
886	92.5	5.5	606	4	US-08-467-602-277	Sequence 277, App	959	91.5	5.4	576	3	US-08-173-351A-30	Sequence 30, App1
887	92.5	5.5	606	4	US-08-411-295F-203	Sequence 203, App	960	91.5	5.4	576	4	US-08-466-592A-4	Sequence 4, App1
888	92.5	5.5	608	3	US-09-095-385-4	Sequence 4, App1	961	91.5	5.4	576	5	PCT-US94-02414-4	Sequence 4, App1
889	92.5	5.5	653	4	US-08-467-602-275	Sequence 275, App	962	91.5	5.4	576	5	PCT-US96-08899-4	Sequence 4, App1
890	92.5	5.5	653	4	US-08-411-295F-201	Sequence 201, App	963	91.5	5.4	644	3	PCT-US93-00031-19	Sequence 19, App1
891	92.5	5.5	746	3	US-08-434-000A-4	Sequence 4, App1	964	91.5	5.4	644	5	PCT-US93-00031-21	Sequence 21, App1
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895	92	5.5	274	4	US-09-813-659-30	Sequence 30, App1	968	91.5	5.4	647	5	PCT-US93-00031-17	Sequence 23, App1
896	92	5.5	274	4	US-09-549-067A-30	Sequence 30, App1	969	91.5	5.4	740	5	PCT-US93-00031-123	Sequence 17, App1
897	92	5.5	302	1	US-08-121-054C-18	Sequence 18, App1	970	91.5	5.4	1241	3	US-09-040-774-2	Sequence 2, App1
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901	92	5.5	302	4	US-09-813-659-18	Sequence 18, App1	974	91.5	5.4	1911	5	PCT-US94-10166-5	Sequence 5, App1
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982	91	5.4	556	1	US-08-471-570-4	Sequence 2, App1	1055	88.5	5.2	135	2	US-08-454-236-2	Sequence 2, App1
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985	91	5.4	581	4	US-09-499-522-18	Sequence 18, App1	1058	88	5.2	181	3	US-08-753-007A-4	Sequence 4, App1
986	91	5.4	581	4	US-09-269-939A-12	Sequence 12, App1	1059	88	5.2	181	3	US-09-398-496-4	Sequence 4, App1
987	91	5.4	619	4	US-08-467-602-233	Sequence 233, App	1060	88	5.2	224	4	US-09-530-139-38	Sequence 38, App1
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989	91	5.4	652	1	US-08-471-570-10	Sequence 10, App1	1062	88	5.2	407	3	US-08-753-007A-6	Sequence 6, App1
990	91	5.4	816	1	US-07-640-029-1	Sequence 11, App1	1063	88	5.2	407	3	US-09-398-496-6	Sequence 6, App1
991	90.5	5.4	76	4	US-09-397-243D-11	Sequence 11, App1	1064	88	5.2	421	4	US-09-569-619C-35	Sequence 36, App1
992	90.5	5.4	310	3	US-08-477-660B-6	Sequence 6, App1	1065	88	5.2	490	4	US-09-963-137-199	Sequence 199, App
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994	90.5	5.4	310	3	US-09-329-916-6	Sequence 6, App1	1067	88	5.2	605	3	US-08-753-007A-2	Sequence 2, App1
995	90.5	5.4	310	3	US-08-485-372A-6	Sequence 6, App1	1068	88	5.2	605	3	US-09-398-496-2	Sequence 2, App1
996	90.5	5.4	310	3	US-09-409-006A-6	Sequence 6, App1	1069	88	5.2	605	3	US-09-707-802-8	Sequence 8, App1
997	90.5	5.4	310	4	US-08-484-681-6	Sequence 6, App1	1070	88	5.2	605	3	US-09-991-326-8	Sequence 8, App1
998	90.5	5.4	310	4	US-09-766-995-6	Sequence 6, App1	1071	88	5.2	731	4	US-09-910-174B-15	Sequence 15, App1
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1002	90.5	5.4	754	2	US-08-525-864A-2	Sequence 2, App1	1075	87.5	5.2	205	1	US-08-233-005-2	Sequence 2, App1
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1005	90	5.3	240	3	US-09-296-595-8	Sequence 8, App1	1078	87.5	5.2	205	3	PCT-US95-04858-2	Sequence 2, App1
1006	90	5.3	288	4	US-09-651-200-14	Sequence 14, App1	1079	87.5	5.2	386	4	US-08-467-602-218	Sequence 218, App
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1009	90	5.3	335	4	US-08-411-295F-153	Sequence 153, App	1082	87.5	5.2	420	1	US-08-456-201-29	Sequence 29, App1
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1013	90	5.3	433	2	US-08-808-374-1	Sequence 1, App1	1086	87.5	5.2	420	5	PCT-US92-04295A-29	Sequence 29, App1
1014	90	5.3	434	3	US-09-540-445A-19	Sequence 19, App1	1087	87.5	5.2	473	3	US-09-828-995B-20	Sequence 20, App1
1015	90	5.3	453	2	US-08-661-052-16	Sequence 16, App1	1088	87.5	5.2	603	4	US-08-467-602-216	Sequence 216, App1
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1023	90	5.3	582	4	US-09-589-184-334	Sequence 334, App	1096	87.5	5.2	650	4	US-08-467-602-217	Sequence 217, App
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1028	90	5.3	646	4	US-08-467-602-270	Sequence 270, App	1101	87	5.2	349	3	US-08-470-335-188	Sequence 188, App
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1035	90	5.3	821	3	US-08-323-430-13	Sequence 13, App1	1108	87	5.2	771	3	US-08-434-000A-8	Sequence 8, App1
1036	90	5.3	1018	1	US-08-408-093-6	Sequence 6, App1	1109	87	5.2	771	3	US-09-312-157-8	Sequence 8, App1
1037	90	5.3	1018	1	US-08-408-420A-6	Sequence 6, App1	1110	86.5	5.1	90	2	US-08-454-236-4	Sequence 4, App1
1038	90	5.3	1018	1	US-08-714-901-6	Sequence 6, App1	1111	86.5	5.1	218	3	PCT-US94-14106-57	Sequence 57, App1
1039	90	5.3	1018	3	US-08-040-741-6	Sequence 6, App1	1112	86.5	5.1	230	3	US-09-485-737B-102	Sequence 102, App
1040	89.5	5.3	1170	4	US-09-260-527-1	Sequence 1, App1	1113	86.5	5.1	395	4	US-08-467-602-290	Sequence 290, App
1041	89.5	5.3	1170	4	US-09-749-588-2	Sequence 2, App1	1114	86.5	5.1	395	4	US-08-411-295F-216	Sequence 216, App
1042	89.5	5.3	93	3	US-08-928-383B-19	Sequence 19, App1	1115	86.5	5.1	612	4	US-08-467-602-291	Sequence 291, App
1043	89	5.3	287	4	US-09-800-729-114	Sequence 114, App1	1116	86.5	5.1	612	4	US-08-411-295F-217	Sequence 217, App
1044	89	5.3	287	4	US-09-800-729-153	Sequence 153, App	1117	86.5	5.1	659	4	US-08-467-602-292	Sequence 292, App
1045	89	5.3	287	4	US-09-486-814A-27	Sequence 27, App1	1118	86.5	5.1	659	4	US-08-411-295F-218	Sequence 218, App
1047	89	5.3	322	4	US-09-684-708A-27	Sequence 27, App1	1119	86.5	5.1	826	4	US-09-071-035-264	Sequence 264, App
1048	89	5.3	466	2	US-08-432-016-4	Sequence 4, App1	1120	86.5	5.1	826	4	US-09-877-730-16	Sequence 16, App1
1049	89	5.3	466	2	US-08-684-594-4	Sequence 4, App1	1121	86.5	5.1	885	1	US-08-372-892-4	Sequence 4, App1
							1122	86.5	5.1	885	4	US-09-919-497-52	Sequence 52, App1

1123	86.5	5.1	894	1	US-08-372-892-2	Sequence 2, Appl1	1196	84.5	5.0	457	1	US-08-416-478A-8	Sequence 8, Appl1
1124	86.5	5.1	894	1	US-08-445-640-34	Sequence 34, Appl1	1197	84.5	5.0	457	2	US-08-474-988B-8	Sequence 8, Appl1
1125	86.5	5.1	894	3	US-08-170-558-34	Sequence 34, Appl1	1198	84.5	5.0	457	2	US-08-394-442B-8	Sequence 8, Appl1
1126	86.5	5.1	894	3	US-08-447-314-34	Sequence 34, Appl1	1199	84.5	5.0	524	4	US-09-270-747-44009	Sequence 44009, A
1127	86.5	5.1	894	3	US-08-445-461-34	Sequence 34, Appl1	1200	84	5.0	223	3	US-08-811-682-8	Sequence 8, Appl1
1128	86.5	5.1	904	4	US-09-877-730-6	Sequence 6, Appl1	1201	84	5.0	230	4	US-08-467-602-223	Sequence 223, App
1129	86.5	5.1	907	4	US-09-877-730-30	Sequence 20, Appl1	1202	84	5.0	230	4	US-08-411-295F-119	Sequence 149, App
1130	86.5	5.1	985	4	US-09-877-730-10	Sequence 10, Appl1	1203	84	5.0	241	2	US-08-324-591-18	Sequence 18, App
1131	86.5	5.1	991	4	US-09-877-730-12	Sequence 12, Appl1	1204	84	5.0	241	2	US-08-326-789-18	Sequence 18, App
1132	86.5	5.1	1018	4	US-08-452-052-2	Sequence 2, Appl1	1205	84	5.0	245	3	US-09-069-821-5	Sequence 5, Appl1
1133	86.5	5.1	1069	4	US-09-877-730-2	Sequence 2, Appl1	1206	84	5.0	245	4	US-09-956-086-5	Sequence 5, Appl1
1134	86.5	5.1	1072	4	US-09-877-730-18	Sequence 18, Appl1	1207	84	5.0	245	4	US-09-956-087-5	Sequence 5, Appl1
1135	86.5	5.1	1150	4	US-09-877-730-8	Sequence 8, Appl1	1208	84	5.0	264	4	US-08-467-602-265	Sequence 265, App
1136	86.5	5.1	1363	4	US-09-375-248-19	Sequence 19, Appl1	1209	84	5.0	264	4	US-08-411-295F-191	Sequence 191, App
1137	86	5.1	241	3	US-08-341-018-54	Sequence 53, Appl1	1210	84	5.0	265	4	US-09-420-592A-5	Sequence 5, Appl1
1138	86	5.1	241	3	US-08-470-335-195	Sequence 195, App	1211	84	5.0	265	4	US-09-985-442-5	Sequence 5, Appl1
1139	86	5.1	241	3	US-08-470-339-195	Sequence 195, App	1212	84	5.0	265	4	US-09-983-580-5	Sequence 5, Appl1
1140	86	5.1	241	4	US-08-467-602-189	Sequence 189, App	1213	84	5.0	323	4	US-09-684-708A-25	Sequence 25, Appl1
1141	86	5.1	241	4	US-08-411-295F-47	Sequence 47, Appl1	1214	84	5.0	386	4	US-08-467-602-281	Sequence 281, App
1142	86	5.1	270	2	US-08-652-507-2	Sequence 2, Appl1	1215	84	5.0	386	4	US-08-411-295F-207	Sequence 207, App
1143	86	5.1	398	1	US-08-091-519-2	Sequence 2, Appl1	1216	84	5.0	450	3	US-08-811-682-2	Sequence 2, Appl1
1144	86	5.1	398	1	US-08-442-043A-2	Sequence 2, Appl1	1217	84	5.0	530	3	US-08-477-460B-4	Sequence 4, Appl1
1145	86	5.1	398	3	US-09-173-151A-26	Sequence 26, Appl1	1218	84	5.0	530	3	US-08-479-516-4	Sequence 4, Appl1
1146	86	5.1	398	4	US-09-461-908-2	Sequence 2, Appl1	1219	84	5.0	530	3	US-09-329-916-4	Sequence 4, Appl1
1147	86	5.1	398	4	US-08-441-893A-2	Sequence 2, Appl1	1220	84	5.0	530	3	US-08-485-372A-4	Sequence 4, Appl1
1148	86	5.1	398	4	US-08-406-824A-8	Sequence 8, Appl1	1221	84	5.0	530	3	US-09-409-006A-4	Sequence 4, Appl1
1149	86	5.1	398	4	US-09-921-667-8	Sequence 8, Appl1	1222	84	5.0	530	4	US-08-484-681-4	Sequence 4, Appl1
1150	86	5.1	398	4	PCT-US91-03478-2	Sequence 2, Appl1	1223	84	5.0	530	4	US-09-766-995-4	Sequence 4, Appl1
1151	86	5.1	483	3	US-09-310-463-16	Sequence 16, Appl1	1224	84	5.0	530	5	PCT-US93-07422-4	Sequence 4, Appl1
1152	86	5.1	483	4	US-08-842-248A-16	Sequence 16, Appl1	1225	84	5.0	603	4	US-08-467-602-279	Sequence 279, App
1153	86	5.1	579	3	US-09-173-151A-2	Sequence 2, Appl1	1226	84	5.0	603	4	US-08-411-295F-205	Sequence 205, App
1154	86	5.1	630	4	US-09-499-522-16	Sequence 2, Appl1	1227	84	5.0	630	4	US-08-467-602-280	Sequence 280, App
1155	86	5.1	630	4	US-09-269-939A-10	Sequence 10, Appl1	1228	84	5.0	630	4	US-08-411-295F-206	Sequence 206, App
1156	86	5.1	686	3	US-09-173-151A-4	Sequence 4, Appl1	1229	83.5	4.9	100	4	US-09-858-664A-25	Sequence 25, Appl1
1157	86	5.1	1434	4	US-10-080-505-9	Sequence 9, Appl1	1230	83.5	4.9	100	4	US-10-274-978-26	Sequence 26, Appl1
1158	85.5	5.1	225	4	US-09-530-139-42	Sequence 42, Appl1	1231	83.5	4.9	211	1	US-08-168-091A-4	Sequence 4, Appl1
1159	85.5	5.1	300	1	US-07-640-029-5	Sequence 5, Appl1	1232	83.5	4.9	211	1	US-08-335-83A-5	Sequence 5, Appl1
1160	85.5	5.1	300	3	US-08-439-992A-5	Sequence 5, Appl1	1233	83.5	4.9	211	2	US-08-465-473B-5	Sequence 5, Appl1
1161	85.5	5.1	302	1	US-07-640-029-6	Sequence 6, Appl1	1234	83.5	4.9	288	2	US-08-147-772-2	Sequence 2, Appl1
1162	85.5	5.1	302	1	US-07-921-807B-7	Sequence 7, Appl1	1235	83.5	4.9	288	2	US-08-456-104-6	Sequence 6, Appl1
1163	85.5	5.1	302	1	US-07-921-807B-8	Sequence 8, Appl1	1236	83.5	4.9	288	2	US-08-101-624-23	Sequence 23, Appl1
1164	85.5	5.1	302	1	US-08-441-944A-7	Sequence 7, Appl1	1237	83.5	4.9	288	2	US-08-751-667A-6	Sequence 6, Appl1
1165	85.5	5.1	302	1	US-08-441-944A-8	Sequence 8, Appl1	1238	83.5	4.9	288	3	US-08-153-262-2	Sequence 2, Appl1
1166	85.5	5.1	302	1	US-08-439-992A-6	Sequence 6, Appl1	1239	83.5	4.9	288	3	US-08-479-744A-29	Sequence 29, Appl1
1167	85.5	5.1	312	3	US-09-079-029-10	Sequence 10, Appl1	1240	83.5	4.9	288	3	US-08-280-757B-29	Sequence 29, Appl1
1168	85.5	5.1	335	4	US-09-252-991A-27567	Sequence 27567, A	1241	83.5	4.9	288	3	US-09-159-135-2	Sequence 19, Appl1
1169	85.5	5.1	403	4	US-09-638-649-5	Sequence 5, Appl1	1242	83.5	4.9	288	3	US-08-205-697A-19	Sequence 19, Appl1
1170	85.5	5.1	615	4	US-08-840-713-35	Sequence 35, Appl1	1243	83.5	4.9	288	3	US-08-702-525-19	Sequence 19, Appl1
1171	85.5	5.1	617	4	US-08-840-713-37	Sequence 37, Appl1	1244	83.5	4.9	288	3	US-09-450-198-2	Sequence 2, Appl1
1172	85.5	5.1	741	4	US-09-585-858-11	Sequence 11, Appl1	1245	83.5	4.9	288	3	US-08-403-253A-2	Sequence 2, Appl1
1173	85.5	5.1	1665	4	US-09-858-664A-2	Sequence 2, Appl1	1246	83.5	4.9	288	4	US-09-651-000-13	Sequence 13, Appl1
1174	85.5	5.1	1665	4	US-10-274-978-2	Sequence 2, Appl1	1247	83.5	4.9	288	4	US-09-667-135-34	Sequence 34, Appl1
1175	85.5	5.1	2315	4	US-09-543-681A-5434	Sequence 5434, App	1248	83.5	4.9	288	4	US-08-435-816A-2	Sequence 2, Appl1
1176	85	5.0	140	3	US-08-986-485-4	Sequence 4, Appl1	1249	83.5	4.9	288	4	US-09-425-862-29	Sequence 29, Appl1
1177	85	5.0	247	5	PCT-US94-10257A-2	Sequence 4, Appl1	1250	83.5	4.9	288	4	US-09-837-867A-19	Sequence 19, Appl1
1178	85	5.0	328	1	US-08-225-477B-5	Sequence 5, Appl1	1251	83.5	4.9	288	4	US-09-910-174B-5	Sequence 5, Appl1
1179	85	5.0	328	5	PCT-US95-04353-5	Sequence 5, Appl1	1252	83.5	4.9	288	4	US-09-620-461-5	Sequence 5, Appl1
1180	85	5.0	361	4	US-08-467-602-348	Sequence 248, App	1253	83.5	4.9	288	4	US-08-453-836A-2	Sequence 2, Appl1
1181	85	5.0	361	4	US-08-411-295F-174	Sequence 174, App	1254	83.5	4.9	288	4	US-09-206-132-6	Sequence 6, Appl1
1182	85	5.0	398	4	US-09-579-845-4	Sequence 4, Appl1	1255	83.5	4.9	288	5	PCT-US95-02576-19	Sequence 19, Appl1
1183	85	5.0	578	4	US-08-467-602-249	Sequence 249, App	1256	83.5	4.9	307	2	US-08-332-562A-83	Sequence 83, Appl1
1184	85	5.0	578	4	US-08-411-295F-175	Sequence 175, App	1257	83.5	4.9	307	2	US-08-416-778A-6	Sequence 6, Appl1
1185	85	5.0	625	4	US-08-467-602-550	Sequence 250, App	1258	83.5	4.9	307	2	US-08-474-988B-6	Sequence 6, Appl1
1186	85	5.0	625	4	US-08-411-295F-176	Sequence 176, App	1259	83.5	4.9	307	2	US-08-394-442B-6	Sequence 6, Appl1
1187	85	5.0	769	3	US-08-434-000A-10	Sequence 10, Appl1	1260	83.5	4.9	488	1	US-08-416-478A-9	Sequence 9, Appl1
1188	85	5.0	769	3	US-09-312-157-10	Sequence 10, Appl1	1261	83.5	4.9	488	2	US-08-474-988B-9	Sequence 9, Appl1
1189	85	5.0	2409	6	5180808-2	Patent No. 5180808	1262	83.5	4.9	488	2	US-08-394-442B-9	Sequence 9, Appl1
1190	84.5	5.0	119	4	US-09-858-664A-30	Sequence 30, Appl1	1263	83.5	4.9	530	4	US-08-840-713-2	Sequence 2, Appl1
1191	84.5	5.0	119	4	US-10-274-978-31	Sequence 31, Appl1	1264	83.5	4.9	637	1	US-08-235-83B-14	Sequence 14, Appl1
1192	84.5	5.0	241	4	US-08-411-295F-94	Sequence 94, Appl1	1265	83.5	4.9	637	2	US-08-465-473B-14	Sequence 14, Appl1
1193	84.5	5.0	249	2	US-08-797-689-18	Sequence 18, Appl1	1266	83.5	4.9	711	1	US-08-235-83B-7	Sequence 7, Appl1
1194	84.5	5.0	249	4	US-09-984-186-18	Sequence 18, Appl1	1267	83.5	4.9	711	2	US-08-465-473B-7	Sequence 7, Appl1
1195	84.5	5.0	419	6	5169835-2	Patent No. 5169835	1268	83.5	4.9	729	1	US-08-070-165F-6	Sequence 6, Appl1

1269	83.5	4.9	729	2	US-08-865-418-6	Sequence 6, Appl1	1342	82.5	4.9	253	3	US-09-166-093-17	Sequence 17, Appl1
1270	83.5	4.9	731	1	US-08-070-165F-10	Sequence 10, Appl1	1343	82.5	4.9	253	3	US-09-172-019-17	Sequence 17, Appl1
1271	83.5	4.9	731	2	US-08-885-418-10	Sequence 10, Appl1	1344	82.5	4.9	253	3	US-09-166-094-17	Sequence 17, Appl1
1272	83.5	4.9	1151	4	US-09-710-379-2448	Sequence 2448, Ap	1345	82.5	4.9	253	4	US-09-443-213-17	Sequence 17, Appl1
1273	83.5	4.9	1154	3	US-09-134-001C-3448	Sequence 3428, Ap	1346	82.5	4.9	329	4	US-09-651-200-18	Sequence 18, Appl1
1274	83.5	4.9	3838	2	US-08-876-991-2	Sequence 2, Appl1	1347	82.5	4.9	329	4	US-09-503-040-6	Sequence 6, Appl1
1275	83.5	4.9	3898	2	US-09-059-853-2	Sequence 2, Appl1	1348	82.5	4.9	352	4	US-08-467-602-239	Sequence 239, App
1276	83	4.9	222	2	US-08-190-199A-67	Sequence 67, Appl1	1349	82.5	4.9	352	4	US-08-411-295F-165	Sequence 165, App
1277	83	4.9	223	4	US-09-248-796A-23094	Sequence 23094, A	1350	82.5	4.9	449	2	US-08-482-090-11	Sequence 11, Appl1
1278	83	4.9	237	2	US-08-224-591-16	Sequence 16, Appl1	1351	82.5	4.9	450	1	US-08-105-710-7	Sequence 7, Appl1
1279	83	4.9	237	2	US-08-468-252-5	Sequence 5, Appl1	1352	82.5	4.9	450	1	US-08-365-901-7	Sequence 7, Appl1
1280	83	4.9	237	2	US-08-926-789-16	Sequence 16, Appl1	1353	82.5	4.9	450	2	US-09-007-383-15	Sequence 15, Appl1
1281	83	4.9	237	3	US-08-668-706B-5	Sequence 5, Appl1	1354	82.5	4.9	450	3	US-08-479-703A-6	Sequence 6, Appl1
1282	83	4.9	237	5	PCT-US95-10740-5	Sequence 5, Appl1	1355	82.5	4.9	504	4	US-09-270-767-44344	Sequence 43244, A
1283	83	4.9	238	4	US-09-149-476-485	Sequence 485, Appl	1356	82.5	4.9	538	4	US-09-270-767-44083	Sequence 44083, A
1284	83	4.9	241	1	US-07-847-743B-30	Sequence 30, Appl1	1357	82.5	4.9	551	4	US-08-896-537A-2	Sequence 2, Appl1
1285	83	4.9	241	1	US-08-456-201-30	Sequence 30, Appl1	1358	82.5	4.9	569	4	US-08-667-602-237	Sequence 237, App
1286	83	4.9	241	2	US-08-456-241-30	Sequence 30, Appl1	1359	82.5	4.9	569	4	US-08-411-295F-163	Sequence 163, App
1287	83	4.9	241	5	PCT-US92-04295A-30	Sequence 30, Appl1	1360	82.5	4.9	616	4	US-08-467-602-238	Sequence 238, App
1288	83	4.9	273	4	US-09-270-767-32843	Sequence 32843, A	1361	82.5	4.9	616	4	US-08-411-295F-164	Sequence 164, App
1289	83	4.9	273	4	US-09-270-767-48060	Sequence 48060, A	1362	82.5	4.9	645	3	US-08-753-007A-10	Sequence 10, Appl1
1290	83	4.9	280	3	US-08-341-018-56	Sequence 56, Appl1	1363	82.5	4.9	645	3	US-09-398-496-10	Sequence 10, Appl1
1291	83	4.9	280	3	US-08-470-335-192	Sequence 192, App	1364	82.5	4.9	710	3	US-09-171-461-16	Sequence 16, Appl1
1292	83	4.9	280	3	US-08-470-339-192	Sequence 192, App	1365	82.5	4.9	710	4	US-09-970-711-16	Sequence 16, Appl1
1293	83	4.9	280	4	US-08-467-602-386	Sequence 386, App	1366	82.5	4.9	757	3	US-08-434-000A-6	Sequence 6, Appl1
1294	83	4.9	280	4	US-08-411-295F-49	Sequence 49, Appl1	1367	82.5	4.9	757	3	US-09-312-157-6	Sequence 6, Appl1
1295	83	4.9	281	4	US-08-487-748A-9	Sequence 9, Appl1	1368	82	4.9	210	4	US-08-467-602-215	Sequence 215, App
1296	83	4.9	281	1	US-08-487-748A-10	Sequence 10, Appl1	1369	82	4.9	210	4	US-08-411-295F-141	Sequence 141, App
1297	83	4.9	281	1	US-08-480-070C-10	Sequence 10, Appl1	1370	82	4.9	226	4	US-09-869-388-10	Sequence 10, Appl1
1298	83	4.9	281	3	US-08-829-525-10	Sequence 10, Appl1	1371	82	4.9	244	4	US-08-467-602-257	Sequence 257, App
1299	83	4.9	281	3	US-08-609-583A-10	Sequence 10, Appl1	1372	82	4.9	244	4	US-08-411-295F-183	Sequence 183, App
1300	83	4.9	281	3	US-08-317-399-10	Sequence 10, Appl1	1373	82	4.9	290	4	US-09-910-174B-8	Sequence 8, Appl1
1301	83	4.9	281	4	US-09-310-367-10	Sequence 10, Appl1	1374	82	4.9	290	4	US-09-620-461-8	Sequence 8, Appl1
1302	83	4.9	281	4	US-09-032-337-10	Sequence 10, Appl1	1375	82	4.9	474	4	US-09-828-995B-17	Sequence 17, Appl1
1303	83	4.9	281	4	US-09-464-231-10	Sequence 10, Appl1	1376	82	4.9	522	4	US-09-549-513-33	Sequence 33, Appl1
1304	83	4.9	321	3	US-09-361-434-17	Sequence 17, Appl1	1377	82	4.9	530	3	US-08-983-035A-18	Sequence 38, Appl1
1305	83	4.9	321	3	US-09-361-434-22	Sequence 22, Appl1	1378	82	4.9	595	4	US-09-520-781-12	Sequence 12, Appl1
1306	83	4.9	321	3	US-09-635-025-17	Sequence 17, Appl1	1379	82	4.9	661	2	US-08-795-866-14	Sequence 14, Appl1
1307	83	4.9	321	3	US-09-635-025-22	Sequence 22, Appl1	1380	82	4.9	661	3	US-09-303-069-14	Sequence 14, Appl1
1308	83	4.9	321	4	US-09-479-614-29	Sequence 29, Appl1	1381	82	4.9	661	3	US-09-134-250-14	Sequence 14, Appl1
1309	83	4.9	370	4	US-09-222-938A-64	Sequence 64, Appl1	1382	81.5	4.8	214	4	US-09-247-325-4	Sequence 4, Appl1
1310	83	4.9	431	4	US-09-479-614-14	Sequence 14, Appl1	1383	81.5	4.8	214	4	US-09-466-635-4	Sequence 4, Appl1
1311	83	4.9	445	4	US-09-583-110-4414	Sequence 4414, Ap	1384	81.5	4.8	239	3	US-08-279-772A-8	Sequence 8, Appl1
1312	83	4.9	445	4	US-09-479-614-2	Sequence 2, Appl1	1385	81.5	4.8	239	3	US-08-902-486-11	Sequence 11, Appl1
1313	83	4.9	496	4	US-09-479-614-29	Sequence 29, Appl1	1386	81.5	4.8	268	4	US-09-976-118-1	Sequence 1, Appl1
1314	83	4.9	498	4	US-09-354-151-2	Sequence 2, Appl1	1387	81.5	4.8	326	4	US-09-248-796A-14157	Sequence 14157, A
1315	83	4.9	539	1	US-08-463-163-3	Sequence 3, Appl1	1388	81.5	4.8	602	2	US-08-795-868-16	Sequence 16, Appl1
1316	83	4.9	645	1	US-07-847-743B-27	Sequence 27, Appl1	1389	81.5	4.8	602	3	US-09-303-069-16	Sequence 16, Appl1
1317	83	4.9	645	1	US-08-456-201-27	Sequence 27, Appl1	1390	81.5	4.8	661	1	US-09-134-250-16	Sequence 12, Appl1
1318	83	4.9	645	1	US-08-428-926-4	Sequence 4, Appl1	1391	81.5	4.8	661	1	US-08-232-538-12	Sequence 12, Appl1
1319	83	4.9	645	1	US-08-428-927-4	Sequence 4, Appl1	1392	81.5	4.8	661	2	US-08-786-164-11	Sequence 6, Appl1
1320	83	4.9	645	1	US-08-428-928-4	Sequence 4, Appl1	1393	81.5	4.8	687	1	US-08-232-538-6	Sequence 6, Appl1
1321	83	4.9	645	1	US-08-339-517-4	Sequence 27, Appl1	1394	81.5	4.8	687	2	US-08-786-164-6	Sequence 2, Appl1
1322	83	4.9	645	2	US-08-456-241-27	Sequence 27, Appl1	1395	81.5	4.8	1188	1	US-09-427-353-2	Sequence 4, Appl1
1323	83	4.9	645	3	US-09-020-880-93	Sequence 93, Appl1	1396	81.5	4.8	87	4	US-08-201-697-4	Sequence 29, Appl1
1324	83	4.9	645	3	US-09-101-544-93	Sequence 93, Appl1	1397	81	4.8	87	4	US-08-858-664A-29	Sequence 30, Appl1
1325	83	4.9	645	4	US-09-097-681-3	Sequence 3, Appl1	1398	81	4.8	87	4	US-10-274-978-30	Sequence 30, Appl1
1326	83	4.9	645	5	PCT-US92-04295A-27	Sequence 27, Appl1	1399	81	4.8	227	4	US-09-869-388-6	Sequence 6, Appl1
1327	83	4.9	732	1	US-07-847-743B-9	Sequence 9, Appl1	1400	81	4.8	235	3	US-09-485-737B-93	Sequence 93, Appl1
1328	83	4.9	732	2	US-08-456-201-9	Sequence 9, Appl1	1401	81	4.8	239	4	US-09-828-995B-26	Sequence 26, Appl1
1329	83	4.9	732	2	US-08-456-241-9	Sequence 9, Appl1	1402	81	4.8	401	6	US-08-828-995B-26	Sequence 26, Appl1
1330	83	4.9	732	5	PCT-US92-04295A-9	Sequence 9, Appl1	1403	81	4.8	945	4	US-09-291-299A-3	Sequence 3, Appl1
1331	82.5	4.9	718	4	US-10-026-045-1	Sequence 1, Appl1	1404	81	4.8	945	4	US-10-140-000-146	Sequence 146, App
1332	82.5	4.9	244	1	US-08-230-843-2	Sequence 2, Appl1	1405	80.5	4.8	90	3	US-08-928-388B-22	Sequence 22, Appl1
1333	82.5	4.9	244	2	US-08-636-936-2	Sequence 15, Appl1	1406	80.5	4.8	129	4	US-09-556-605-2	Sequence 33, Appl1
1334	82.5	4.9	250	2	US-08-392-338A-15	Sequence 15, Appl1	1407	80.5	4.8	165	1	US-08-168-091A-33	Sequence 32640, A
1335	82.5	4.9	250	3	US-09-166-750-15	Sequence 15, Appl1	1408	80.5	4.8	191	4	US-09-270-767-33640	Sequence 2, Appl1
1336	82.5	4.9	250	3	US-09-166-093-15	Sequence 15, Appl1	1409	80.5	4.8	206	3	US-08-341-018-2	Sequence 190, App
1337	82.5	4.9	250	3	US-09-172-019-15	Sequence 15, Appl1	1410	80.5	4.8	206	3	US-08-470-333-180	Sequence 190, App
1338	82.5	4.9	250	3	US-09-166-094-15	Sequence 15, Appl1	1411	80.5	4.8	206	3	US-08-470-333-180	Sequence 190, App
1339	82.5	4.9	250	4	US-09-443-213-15	Sequence 15, Appl1	1412	80.5	4.8	206	4	US-08-467-602-353	Sequence 383, App
1340	82.5	4.9	253	2	US-08-392-338A-17	Sequence 17, Appl1	1413	80.5	4.8	206	4	US-08-411-295F-2	Sequence 2, Appl1
1341	82.5	4.9	253	3	US-09-166-750-17	Sequence 17, Appl1	1414	80.5	4.8	206	4	US-08-411-295F-76	Sequence 76, Appl1

Db 241 TEAPTTMYPLKATSTVKOSWDTTMDGYLGETSAGPKSLPVFAIIILISLCMVVFT 300
QY 301 MAIIMLCRTSQOEHYEAR 321
Db 301 MAIIMLCRTSQOEHYEAR 321

RESULT 2

US-09-369-247-63
; Sequence 63, Application US/09369247
; Patent No. 6563992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; EARLIER FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (306)
; OTHER INFORMATION: Xaa equals stop translation
US-09-369-247-63

Query Match

Best Local Similarity 67.4%; Score 1137; DB 4; Length 306;
Matches 226; Conservative 0; Mismatches 1; Indels 94; Gaps 1;

QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGVNLPCTYDPLQGYTVLVKMLVGR 60
Db 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGVNLPCTYDPLQGYTVLVKMLVGR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLSLSTLEMDRSHYTCVWTQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLSLSTLEMDRSHYTCVWTQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKRTVTGSGYGTVAQMKRISLQCCARSGSPISYIMYKQ 180
Db 121 DGNQVVRDKITELRVQ----- 136
QY 181 QTNNOPIKAVATLSTLLFKPAVIADSGSYFCTAKAGVSGEHSIDIYFVKVDSKLLTKTK 240
Db 137 -----KISSKLLTKTK 146
QY 241 TEAPTTMYPLKATSTVKOSWDTTMDGYLGETSAGPKSLPVFAIIILISLCMVVFT 300
Db 147 TEAPTTMYPLKATSTVKOSWDTTMDGYLGETSAGPKSLPVFAIIILISLCMVVFT 206
QY 301 MAIIMLCRTSQOEHYEAR 321
Db 207 MAIIMLCRTSQOEHYEAR 227

RESULT 3
US-09-188-930-189
; Sequence 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:

; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Marison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)...(247)
; NAME/KEY: UNSURE
; LOCATION: (289)...(289)
US-09-188-930-189

Query Match

Best Local Similarity 10.6%; Score 178.5; DB 3; Length 299;
Matches 65; Conservative 26.5%; Pred. No. 7.3e-10;
Matches 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGVNLPCTYDPLQGYTVLVKMLVGR 60
Db 17 LAILLCSLALGSVTVSH--SEPERIPE-----NPVKLSCAV---SGPSPRVEN----- 62
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHK-----VPDVSLSLSTLEMDRSHYTCV 115
Db 63 -----KPDGSDTRIVLCYNNKKTASVEDRVFPLFGIIFPKSVTRB--DNGYTCMV 111
QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKRTVTGSGYGTVAQMKRISLQCCARSGSPIS 174
Db 112 SEEGNSYGEVAKLIVL-----VPSKPTVNIIPS-----SATIGNRAVLTCSEDDGSPPE 163
QY 175 YIMYK-----QQTN-----NOEPIKAVATLSTLLFKPAVIADSGSYFCTAKAGVSGEQH 222
Db 164 YTFPKDGIIVPTNPKSTRASNSYVLANPTGELVFDPLASDGTGYSCEARNGYGTPT 223
QY 223 SDIVK 227
Db 224 SNAVR 228

RESULT 4

US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Marison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-331

Query Match
Best Local Similarity 10.6%; Score 178.5; DB 3; Length 299;
Matches 26.5%; Pred. No. 7.3e-10;

LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-189

Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGLHLLTVDTYGRPLIEVESVTPGPKGDVNLPCYTDPLQGYTVLVKLVQR 60
DB 17 LAILLCSLALGSVTVHS--SEPEVRIPEN-----NPVKLSCAI---SGFSPREWE----- 62
QY 61 GSDPVTIIFLRDSSGDHIQQAQYQGRHLVSHK-----VPGDVSQQLSTLEMDRSHYTCVEY 115
DB 63 -----KFDGDDTTLVLCVNNKKTASVEDRVTLPGITRKSQTRR--DIGYTCWV 111
QY 116 TWGTPDGNNOVVRDKITELRVQKLSVSKPTVTTSGSGYFTVPOGMRLSLOQAR--GSPPI 174
DB 112 SEEGSGSYGEVVKYKLIYL-----VPPSKPTVNIPIPS---SATIGNRAVLTCSEQDGSPPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVAITLSTLFRKANVADSGSYFCTAKQVQSEQH 222
DB 164 YIMFKDGIYVPIPNPKSTRAFSNSSYVLANPTTGBLVFDPUSADTGEYSCEARNGYGTPTMT 223
QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 8
US-09-312-283C-331
Sequence 331, Application US/09312283C
Patent No. 6573095

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muriason, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 331
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-331

Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGLHLLTVDTYGRPLIEVESVTPGPKGDVNLPCYTDPLQGYTVLVKLVQR 60
DB 17 LAILLCSLALGSVTVHS--SEPEVRIPEN-----NPVKLSCAI---SGFSPREWE----- 62
QY 61 GSDPVTIIFLRDSSGDHIQQAQYQGRHLVSHK-----VPGDVSQQLSTLEMDRSHYTCVEY 115
DB 63 -----KFDGDDTTLVLCVNNKKTASVEDRVTLPGITRKSQTRR--DIGYTCWV 111
QY 116 TWGTPDGNNOVVRDKITELRVQKLSVSKPTVTTSGSGYFTVPOGMRLSLOQAR--GSPPI 174
DB 112 SEEGSGSYGEVVKYKLIYL-----VPPSKPTVNIPIPS---SATIGNRAVLTCSEQDGSPPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVAITLSTLFRKANVADSGSYFCTAKQVQSEQH 222
DB 164 YIMFKDGIYVPIPNPKSTRAFSNSSYVLANPTTGBLVFDPUSADTGEYSCEARNGYGTPTMT 223

QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 9
US-09-907-794A-119
Sequence 119, Application US/09907794A
Patent No. 6635468

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20

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; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-119

Query Match      10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHLYVDYGRPILEVPESVYGPVKGDVNLPCYTPYLOGYQVLVKMLVQR 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 17 LAILLCSLALGSLVTVHS-SSEPRVIRPEN-----NPVKLSGAY---SGFSPPREV----- 62
QY 61 GSDPVITFLRDSGDHIIQAKYQGRLLVSHK-----VPGDVSLQLSTLEMDRSHYTCEV 115
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 63 -----KFDGDTTRLVLCYNNKITASVEDRVTFLPTGITPKSVTR--DTGYTCMV 111
QY 116 TWQTPDGNQVVRDKITELRVQKLSVKPYTTTSSGYGFTVPQGRISLQCGAR-GSPPI 174
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 112 SEEGNSYGEVKKYKLYLVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEODGSPSE 163
QY 175 YIYWK-----QQTN-----NOEPIKVAITLSTLFFKPAVIADSGSYFCTAKGVGSEQH 222
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 164 YTFKDGIVMPTPKSTRAFSNNSYVLPFTTGLVDFPLSADTGEYSCARNGYGTPTMT 223
QY 223 SDIVK 227
   :|||:
DB 224 SNAVR 228

RESULT 10
US-09-905-125A-119
; Sequence 119, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Batoni, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
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; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-119

Query Match      10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHLYVDYGRPILEVPESVYGPVKGDVNLPCYTPYLOGYQVLVKMLVQR 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 17 LAILLCSLALGSLVTVHS-SSEPRVIRPEN-----NPVKLSGAY---SGFSPPREV----- 62
QY 61 GSDPVITFLRDSGDHIIQAKYQGRLLVSHK-----VPGDVSLQLSTLEMDRSHYTCEV 115
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 63 -----KFDGDTTRLVLCYNNKITASVEDRVTFLPTGITPKSVTR--DTGYTCMV 111
QY 116 TWQTPDGNQVVRDKITELRVQKLSVKPYTTTSSGYGFTVPQGRISLQCGAR-GSPPI 174
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 112 SEEGNSYGEVKKYKLYLVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEODGSPSE 163
QY 175 YIYWK-----QQTN-----NOEPIKVAITLSTLFFKPAVIADSGSYFCTAKGVGSEQH 222
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 164 YTFKDGIVMPTPKSTRAFSNNSYVLPFTTGLVDFPLSADTGEYSCARNGYGTPTMT 223
QY 223 SDIVK 227
   :|||:
DB 224 SNAVR 228

RESULT 11
US-09-902-775A-119
; Sequence 119, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Batoni, Dan L.
; APPLICANT: Ferrara, Napoleone
```

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guirney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-119

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QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 12
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Sequence 3, Application US/09397243D
Patent No. 669688
GENERAL INFORMATION:
APPLICANT: Kornecki, Elizabeth
APPLICANT: Sobocka, Malgorzata B.
TITLE OF INVENTION: Human Platelet P11 Receptor
FILE REFERENCE: 011,00221
CURRENT APPLICATION NUMBER: US/09/397,243D
CURRENT FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: 60/100,638
PRIOR FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-397-243D-3

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RESULT 13
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Sequence 119, Application US/09906700
Patent No. 6721535
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnogyers, Luc
APPLICANT: Eaton, Dan L.

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APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 119
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-906-700-119

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Best Local Similarity 26.5%; Pred. No. 7.3e-10;
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RESULT 14
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Sequence 366, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
PRIOR FILING DATE: 2002-05-06
Prior Application removed - See Palm or File wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 366
LENGTH: 299
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-002-366

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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101	1688	100.0	321	16	US-10-633-008-32	Sequence 32, Appl	174	178.5	10.6	299	10	US-09-904-877A-119	Sequence 119, App
102	1688	100.0	321	16	US-10-656-269-42	Sequence 42, Appl	175	178.5	10.6	299	10	US-09-904-877A-119	Sequence 119, App
103	1480	87.7	281	16	US-10-656-269-44	Sequence 44, Appl	176	178.5	10.6	299	10	US-09-903-562-119	Sequence 119, App
104	1137	67.4	305	16	US-10-633-008-33	Sequence 33, Appl	177	178.5	10.6	299	10	US-09-906-618-119	Sequence 119, App
105	1137	67.4	306	14	US-10-662-548-63	Sequence 63, Appl	178	178.5	10.6	299	10	US-09-907-728-119	Sequence 119, App
106	728	43.1	280	16	US-10-633-008-34	Sequence 34, Appl	179	178.5	10.6	299	10	US-09-904-805-119	Sequence 119, App
107	728	43.1	280	16	US-10-656-269-14	Sequence 14, Appl	180	178.5	10.6	299	10	US-09-904-938A-119	Sequence 119, App
108	613	36.3	188	16	US-10-656-269-16	Sequence 16, Appl	181	178.5	10.6	299	10	US-09-906-722A-119	Sequence 119, App
109	178.5	10.6	299	9	US-09-799-777-51	Sequence 51, Appl	182	178.5	10.6	299	11	US-09-908-576-119	Sequence 119, App
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111	178.5	10.6	299	9	US-09-909-088B-119	Sequence 119, App	184	178.5	10.6	299	11	US-09-833-245-1301	Sequence 1301, Ap
112	178.5	10.6	299	9	US-09-905-291A-119	Sequence 119, App	185	178.5	10.6	299	13	US-10-066-500-91	Sequence 366, App
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114	178.5	10.6	299	9	US-09-902-853-119	Sequence 119, App	187	178.5	10.6	299	14	US-10-140-808-366	Sequence 366, App
115	178.5	10.6	299	9	US-09-907-824-119	Sequence 119, App	188	178.5	10.6	299	14	US-10-121-049-366	Sequence 366, App
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131	178.5	10.6	299	10	US-09-866-050A-331	Sequence 331, App	204	178.5	10.6	299	14	US-10-066-193-91	Sequence 91, Appl
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224	178.5	10.6	299	14	US-10-131-830A-366	Sequence 366, App	307	178.5	10.6	299	14	US-10-127-833A-366	Sequence 366, App
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299	178.5	10.6	299	14	US-10-121-159-366	Sequence 366, App	382	178.5	10.6	299	14	US-10-147-537-366	Sequence 366, App
300	178.5	10.6	299	14	US-10-121-164-366	Sequence 366, App	383	178.5	10.6	299	14	US-10-147-539-366	Sequence 366, App
301	178.5	10.6	299	14	US-10-121-169-366	Sequence 366, App	384	178.5	10.6	299	14	US-10-147-541-366	Sequence 366, App
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382	178.5	10.6	299	14	US-10-137-870-366	Sequence 366, App	455	178.5	10.6	299	14	US-10-147-490-366	Sequence 366, App
383	178.5	10.6	299	14	US-10-140-018-366	Sequence 366, App	456	178.5	10.6	299	14	US-10-147-494-366	Sequence 366, App
384	178.5	10.6	299	14	US-10-140-021-366	Sequence 366, App	457	178.5	10.6	299	14	US-10-147-498-366	Sequence 366, App
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593	178.5	10.6	299	14	US-10-145-749-366	Sequence 366, App	666	178.5	10.6	299	17	US-10-767-374-1	Sequence 1, Appl1
594	178.5	10.6	299	14	US-10-145-753-366	Sequence 366, App	667	178.5	10.6	299	17	US-10-785-607-1	Sequence 366, App
595	178.5	10.6	299	14	US-10-145-871-366	Sequence 366, App	668	178.5	10.6	299	17	US-10-145-961-366	Sequence 366, Appl1
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866	158	352	14	US-10-229-874-216	Sequence 216, App	939	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
867	158	352	14	US-10-230-024-216	Sequence 216, App	940	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
868	158	352	14	US-10-230-113-216	Sequence 216, App	941	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
869	158	352	14	US-10-230-183-216	Sequence 216, App	942	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
870	158	352	14	US-10-230-234-216	Sequence 216, App	943	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
871	158	352	14	US-10-230-306-216	Sequence 216, App	944	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
872	158	352	14	US-10-230-426-216	Sequence 216, App	945	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
873	158	352	14	US-10-230-427-216	Sequence 216, App	946	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
874	158	352	14	US-10-230-433-216	Sequence 216, App	947	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
875	158	352	14	US-10-230-435-216	Sequence 216, App	948	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
876	158	352	14	US-10-230-438-216	Sequence 216, App	949	153.5	9, 1	333	9	US-09-989-828-503	Sequence 503, App
877	158	352	14	US-10-232-222-216	Sequence 216, App	950	153.5	9, 1	333	10	US-09-989-828-503	Sequence 503, App
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886	158	352	14	US-10-223-083-280	Sequence 280, App	959	153.5	9, 1	333	10	US-09-990-433-503	Sequence 503, App
887	158	352	14	US-10-216-166-216	Sequence 216, App	960	153.5	9, 1	333	10	US-09-990-562-503	Sequence 503, App
888	158	352	14	US-10-218-612-216	Sequence 216, App	961	153.5	9, 1	333	10	US-09-990-711-503	Sequence 503, App
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1290	153.5	9.1	373	14	US-10-146-724-388	Sequence 388, App	1363	153.5	9.1	373	14	US-10-152-401-388	Sequence 388, App
1291	153.5	9.1	373	14	US-10-146-725-388	Sequence 388, App	1364	153.5	9.1	373	14	US-10-152-793-388	Sequence 388, App
1292	153.5	9.1	373	14	US-10-146-795-388	Sequence 388, App	1365	153.5	9.1	373	14	US-10-156-752-388	Sequence 388, App
1293	153.5	9.1	373	14	US-10-147-495-388	Sequence 388, App	1366	153.5	9.1	373	14	US-10-156-821-388	Sequence 388, App
1294	153.5	9.1	373	14	US-10-147-501-388	Sequence 388, App	1367	153.5	9.1	373	14	US-10-143-032-388	Sequence 388, App
1295	153.5	9.1	373	14	US-10-147-529-388	Sequence 388, App	1368	153.5	9.1	373	14	US-10-143-032-388	Sequence 388, App
1296	153.5	9.1	373	14	US-10-147-506-388	Sequence 388, App	1369	153.5	9.1	373	14	US-10-145-871-388	Sequence 388, App
1297	153.5	9.1	373	14	US-10-147-509-388	Sequence 388, App	1370	153.5	9.1	373	14	US-10-145-871-388	Sequence 388, App
1298	153.5	9.1	373	14	US-10-147-511-388	Sequence 388, App	1371	153.5	9.1	373	14	US-10-145-827-388	Sequence 388, App
1299	153.5	9.1	373	14	US-10-147-523-388	Sequence 388, App	1372	153.5	9.1	373	14	US-10-145-827-388	Sequence 388, App
1300	153.5	9.1	373	14	US-10-152-329-388	Sequence 388, App	1373	153.5	9.1	373	14	US-10-145-827-388	Sequence 388, App
1301	153.5	9.1	373	14	US-10-152-329-388	Sequence 388, App	1374	153.5	9.1	373	14	US-10-145-827-388	Sequence 388, App
1302	153.5	9.1	373	14	US-10-153-566-388	Sequence 388, App	1375	153.5	9.1	373	14	US-10-145-827-388	Sequence 388, App
1303	153.5	9.1	373	14	US-10-158-786-388	Sequence 388, App	1376	153.5	9.1	373	14	US-10-146-787-388	Sequence 388, App
1304	153.5	9.1	373	14	US-10-143-031A-59	Sequence 59, App1	1377	153.5	9.1	373	14	US-10-146-790-388	Sequence 388, App
1305	153.5	9.1	373	14	US-10-137-870-388	Sequence 388, App	1378	153.5	9.1	373	14	US-10-146-793-388	Sequence 388, App
1306	153.5	9.1	373	14	US-10-137-870-388	Sequence 388, App	1379	153.5	9.1	373	14	US-10-146-793-388	Sequence 388, App
1307	153.5	9.1	373	14	US-10-140-021-388	Sequence 388, App	1380	153.5	9.1	373	14	US-10-147-458-388	Sequence 388, App
1308	153.5	9.1	373	14	US-10-140-427-388	Sequence 388, App	1381	153.5	9.1	373	14	US-10-147-458-388	Sequence 388, App
1309	153.5	9.1	373	14	US-10-140-922-388	Sequence 388, App	1382	153.5	9.1	373	14	US-10-147-467-388	Sequence 388, App
1310	153.5	9.1	373	14	US-10-145-631-388	Sequence 388, App	1383	153.5	9.1	373	14	US-10-147-467-388	Sequence 388, App
1311	153.5	9.1	373	14	US-10-145-631-388	Sequence 388, App	1384	153.5	9.1	373	14	US-10-147-467-388	Sequence 388, App
1312	153.5	9.1	373	14	US-10-158-783-388	Sequence 388, App	1385	153.5	9.1	373	14	US-10-147-467-388	Sequence 388, App
1313	153.5	9.1	373	14	US-10-140-274-388	Sequence 388, App	1386	153.5	9.1	373	14	US-10-147-467-388	Sequence 388, App
1314	153.5	9.1	373	14	US-10-143-030A-59	Sequence 59, App1	1387	153.5	9.1	373	14	US-10-147-467-388	Sequence 388, App
1315	153.5	9.1	373	14	US-10-002-967A-59	Sequence 59, App1	1388	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1316	153.5	9.1	373	14	US-10-017-083A-59	Sequence 59, App1	1389	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1317	153.5	9.1	373	14	US-10-140-019-388	Sequence 388, App	1390	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1318	153.5	9.1	373	14	US-10-140-022-388	Sequence 388, App	1391	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1319	153.5	9.1	373	14	US-10-140-022-388	Sequence 388, App	1392	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1320	153.5	9.1	373	14	US-10-140-862-388	Sequence 388, App	1393	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1321	153.5	9.1	373	14	US-10-141-697-388	Sequence 388, App	1394	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1322	153.5	9.1	373	14	US-10-141-700-388	Sequence 388, App	1395	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1323	153.5	9.1	373	14	US-10-141-700-388	Sequence 388, App	1396	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1324	153.5	9.1	373	14	US-10-141-753-388	Sequence 388, App	1397	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1325	153.5	9.1	373	14	US-10-141-753-388	Sequence 388, App	1398	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1326	153.5	9.1	373	14	US-10-141-758-388	Sequence 388, App	1399	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1327	153.5	9.1	373	14	US-10-142-418-388	Sequence 388, App	1400	153.5	9.1	373	14	US-10-152-379-388	Sequence 388, App
1328	153.5	9.1	373	14	US-10-142-420-388	Sequence 388, App							
1329	153.5	9.1	373	14	US-10-142-420-388	Sequence 388, App							
1330	153.5	9.1	373	14	US-10-142-422-388	Sequence 388, App							
1331	153.5	9.1	373	14	US-10-142-422-388	Sequence 388, App							
1332	153.5	9.1	373	14	US-10-142-422-388	Sequence 388, App							
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1334	153.5	9.1	373	14	US-10-142-422-388	Sequence 388, App							
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1337	153.5	9.1	373	14	US-10-142-422-388	Sequence 388, App							
1338	153.5	9.1	373	14	US-10-142-422-388	Sequence 388							

1401	153.5	9.1	373	14	US-10-152-382-388	Sequence 388, App
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1404	153.5	9.1	373	14	US-10-152-387-388	Sequence 388, App
1405	153.5	9.1	373	14	US-10-152-389-388	Sequence 388, App
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1407	153.5	9.1	373	14	US-10-152-392-388	Sequence 388, App
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1409	153.5	9.1	373	14	US-10-157-784-388	Sequence 388, App
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1411	153.5	9.1	373	14	US-10-158-491-388	Sequence 388, App
1412	153.5	9.1	373	14	US-10-143-028A-59	Sequence 59, Appl
1413	153.5	9.1	373	14	US-10-143-029A-59	Sequence 59, Appl
1414	153.5	9.1	373	14	US-10-142-762-388	Sequence 388, App
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1416	153.5	9.1	373	14	US-10-142-766-388	Sequence 388, App
1417	153.5	9.1	373	14	US-10-145-089A-59	Sequence 59, Appl
1418	153.5	9.1	373	14	US-10-145-625-388	Sequence 388, App
1419	153.5	9.1	373	14	US-10-145-627-388	Sequence 388, App
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1422	153.5	9.1	373	14	US-10-146-789-388	Sequence 388, App
1423	153.5	9.1	373	14	US-10-147-483-388	Sequence 388, App
1424	153.5	9.1	373	14	US-10-147-496-388	Sequence 388, App
1425	153.5	9.1	373	14	US-10-147-505-388	Sequence 388, App
1426	153.5	9.1	373	14	US-10-147-516-388	Sequence 388, App
1427	153.5	9.1	373	14	US-10-152-398-388	Sequence 388, App
1428	153.5	9.1	373	14	US-10-139-980-388	Sequence 388, App
1429	153.5	9.1	373	14	US-10-165-067A-59	Sequence 59, Appl
1430	153.5	9.1	373	14	US-10-145-017A-59	Sequence 59, Appl
1431	153.5	9.1	373	14	US-10-145-750-388	Sequence 388, App
1432	153.5	9.1	373	14	US-10-152-373-388	Sequence 388, App
1433	153.5	9.1	373	14	US-10-164-728A-59	Sequence 59, Appl
1434	153.5	9.1	373	14	US-10-223-081-64	Sequence 64, Appl
1435	153.5	9.1	373	14	US-10-218-765-130	Sequence 130, App
1436	153.5	9.1	373	14	US-10-219-063-130	Sequence 130, App
1437	153.5	9.1	373	14	US-10-219-066-130	Sequence 130, App
1438	153.5	9.1	373	14	US-10-219-067-130	Sequence 130, App
1439	153.5	9.1	373	14	US-10-219-068-130	Sequence 130, App
1440	153.5	9.1	373	14	US-10-219-069-130	Sequence 130, App
1441	153.5	9.1	373	14	US-10-219-073-130	Sequence 130, App
1442	153.5	9.1	373	14	US-10-219-475-130	Sequence 130, App
1443	153.5	9.1	373	14	US-10-219-480-130	Sequence 130, App
1444	153.5	9.1	373	14	US-10-219-483-130	Sequence 130, App
1445	153.5	9.1	373	14	US-10-219-525-130	Sequence 130, App
1446	153.5	9.1	373	14	US-10-219-526-130	Sequence 130, App
1447	153.5	9.1	373	14	US-10-219-530-130	Sequence 130, App
1448	153.5	9.1	373	14	US-10-219-532-130	Sequence 130, App
1449	153.5	9.1	373	14	US-10-219-532-130	Sequence 130, App
1450	153.5	9.1	373	14	US-10-219-533-130	Sequence 130, App
1451	153.5	9.1	373	14	US-10-230-437-130	Sequence 130, App
1452	153.5	9.1	373	14	US-10-232-228-130	Sequence 130, App
1453	153.5	9.1	373	14	US-10-013-926A-59	Sequence 59, Appl
1454	153.5	9.1	373	14	US-10-165-247A-59	Sequence 59, Appl
1455	153.5	9.1	373	14	US-10-145-124A-59	Sequence 59, Appl
1456	153.5	9.1	373	14	US-10-160-502A-59	Sequence 59, Appl
1457	153.5	9.1	373	14	US-10-121-044-388	Sequence 388, App
1458	153.5	9.1	373	14	US-10-121-057-388	Sequence 388, App
1459	153.5	9.1	373	14	US-10-121-057-388	Sequence 388, App
1460	153.5	9.1	373	14	US-10-121-058-388	Sequence 388, App
1461	153.5	9.1	373	14	US-10-121-059-388	Sequence 388, App
1462	153.5	9.1	373	14	US-10-121-060-388	Sequence 388, App
1463	153.5	9.1	373	14	US-10-123-109-388	Sequence 388, App
1464	153.5	9.1	373	14	US-10-123-154-388	Sequence 388, App
1465	153.5	9.1	373	14	US-10-123-157-388	Sequence 388, App
1466	153.5	9.1	373	14	US-10-123-906-388	Sequence 388, App
1467	153.5	9.1	373	14	US-10-124-814-388	Sequence 388, App
1468	153.5	9.1	373	14	US-10-124-816-388	Sequence 388, App
1469	153.5	9.1	373	14	US-10-124-820-388	Sequence 388, App
1470	153.5	9.1	373	14	US-10-125-704-388	Sequence 388, App
1471	153.5	9.1	373	14	US-10-125-927-388	Sequence 388, App
1472	153.5	9.1	373	14	US-10-223-082-64	Sequence 64, Appl
1473	153.5	9.1	373	14	US-10-145-087A-59	Sequence 59, Appl

Search completed: January 4, 2005, 06:24:33
Job time : 561 secs

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GenCore version 5.1.6

OM protein - protein search, using SW model
 Run on: January 4, 2005, 06:10:27 ; Search time 89 Seconds
 (without alignments)
 1293,844 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 1688

Sequence: 1 MGILLGLLLIGHTVDTYGR.....AYIMLCRKTSQEHVYEAAR 321
 Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5
 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_23Sep04.*
 Listing first 1500 summaries

1: geneseqp1980s.*
 2: geneseqp1990s.*
 3: geneseqp2000s.*
 4: geneseqp2001s.*
 5: geneseqp2002s.*
 6: geneseqp2003as.*
 7: geneseqp2003bs.*
 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
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RESULT 1: ID AAY23322 standard; protein; 321 AA.
 DE Amino acid sequence of the PRO362 polypeptide.
 PN WO9927098-A2.
 PD 03-JUN-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 2: ID AAY41691 standard; protein; 321 AA.

DE Human PRO 362 protein sequence.
 PN WO9946281-AZ.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 3: ID AAB33429 standard; protein; 321 AA.

DE Human PRO362 protein UNQ317 SEQ ID NO:80.
 PN WO200053758-A2.
 PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 4: ID AAB44247 standard; protein; 321 AA.

DE Human PRO362 (UNQ317) protein sequence SEQ ID NO:52.
 PN WO200053756-A2.
 PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 5: ID AAY95346 standard; protein; 321 AA.

DE Human PRO362 antitumour protein.
 PN WO2000374638-A2.
 PD 29-JUN-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 6: ID AAB24047 standard; protein; 321 AA.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

DE Human PRO362 protein sequence SEQ ID NO:14.

PN WO200053754-A1.

PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 7: ID ABO25193 standard; protein; 321 AA.

DE Novel human secreted and transmembrane protein PRO362.
 PN US2003050239-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 8: ID ABO72199 standard; protein; 321 AA.

DE Novel human secreted and transmembrane protein PRO362.
 PN US2002192706-A1.
 PD 19-DEC-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 9: ID ABO84879 standard; protein; 321 AA.

DE Human secreted and transmembrane polypeptide PRO362.
 PN US2002177553-A1.
 PD 28-NOV-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 10: ID ABO61077 standard; protein; 321 AA.

DE Human PRO362 polypeptide.
 PN US2002169284-A1.
 PD 14-NOV-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 11: ID ABO80346 standard; protein; 321 AA.

DE Human secreted/transmembrane protein PRO362.
 PN US2003004102-A1.
 PD 02-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 12: ID ABO07737 standard; protein; 321 AA.

DE Human A-33 related antigen PRO362.
 PN US2002182206-A1.
 PD 05-DEC-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 13: ID ADB24591 standard; protein; 321 AA.

DE Novel human secreted and transmembrane protein PRO362.
 PN US2003050241-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 14: ID ABO19648 standard; protein; 321 AA.

DE Novel human secreted and transmembrane protein PRO362.
 PN US2003050240-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1688; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9e-136;

RESULT 15: ID ADA12252 standard; protein; 321 AA.

DE Human secreted/transmembrane polypeptide PRO362.

PN US2003055216-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 16
ID ABO19539 standard; protein; 321 AA.
DE Novel human secreted and transmembrane polypeptide #7.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 17
ID ADB73558 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 18
ID ADB76274 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 19
ID ADC43700 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 20
ID ADC61460 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 21
ID ADC63424 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 22
ID ADC65524 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 23
ID ADC68648 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 24
ID ADC62708 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003068648-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 25
ID ADC67773 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 26
ID ADC41093 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 27
ID ADC67148 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 28
ID ADC62084 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 29
ID ADC41717 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 30
ID ADC78883 standard; protein; 321 AA.
DE Human PRO protein #56.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 31
ID ADE49086 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 32
ID ADE35140 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 33
ID ADE16254 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 34
ID ADD72869 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 35
ID ADD72227 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 36
ID ADE16878 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 37
ID ADF46892 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 38
ID ADG52649 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 39
ID ADG59969 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 40
ID ADH62529 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 41
ID ADI60729 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US200307700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 7; Length 321;
RESULT 42
ID ADE49386 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 43
ID ADE89487 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANT/) PAN J.
PA (PAON/) PAONT N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 44
ID ADF61127 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 45
ID ADF39819 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 46
ID ADF45615 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 47
ID ADE24011 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 48
ID ADE49386 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1688; DB 8; Length 321;
RESULT 49
ID ADE89487 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANT/) PAN J.
PA (PAON/) PAONT N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
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RESULT 48
ID ADF40443 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 49
ID ADF23387 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 50
ID ADF33370 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 51
ID ADF26837 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 52
ID ADF27473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 53
ID ADF41067 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 54
ID ADF3746 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 55
ID ADF25112 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 56
ID ADF26213 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 57
ID ADF27473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;

ID ADF34002 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 58
ID ADF46239 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 59
ID ADG50225 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 60
ID ADG49601 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 61
ID ADG51473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 62
ID ADG48977 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 63
ID ADG48353 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 64
ID ADG50849 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 65
ID ADG58793 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 66
ID ADG62249 standard; protein; 321 AA.

DE Human secreted/cranmembrane protein, PRO362.
PN US200406219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 67
ID ADR25274 standard; protein, 321 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:52.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 68
ID ADM17051 standard; protein, 321 AA.
DE Human secreted/cranmembrane protein, PRO362.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 69
ID ADL06885 standard; protein, 321 AA.
DE Human secreted/cranmembrane protein, PRO362.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 70
ID ADN35285 standard; protein, 321 AA.
DE Human STRIGA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 9e-136;
RESULT 71
ID AAB19396 standard; protein, 399 AA.
DE Amino acid sequence of a human secreted protein.
PN WO2000061755-A2.
PD 19-OCT-2000.
PA (CHIR) CHIRON CORP.
Query Match 100.0%; Score 1688; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 72
ID AAB04230 standard; protein, 399 AA.
DE Human gene 11 encoded secreted protein HMSOM51, SEQ ID NO:85.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 73
ID AAE04208 standard; protein, 399 AA.
DE Human gene 11 encoded secreted protein HMSOM51, SEQ ID NO:63.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 74
ID ABG6448 standard; protein, 399 AA.
DE Human albumin fusion protein #1163.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 5; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 75
ID ABG6448 standard; protein, 399 AA.
DE Human albumin fusion protein #1162.

PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 5; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 76
ID ABU03567 standard; protein, 399 AA.
DE Angiogenesis-associated human protein sequence #112.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 100.0%; Score 1688; DB 6; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 77
ID ADA57183 standard; protein, 399 AA.
DE Human secreted protein #466.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 6; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 78
ID ADA41052 standard; protein, 399 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 6; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 79
ID ABR47904 standard; protein, 399 AA.
DE Human secreted protein, SEQ ID 795.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 6; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 80
ID ABR00157 standard; protein, 399 AA.
DE Human gene 147 encoded secreted protein HSDK49, SEQ ID NO:446.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 6; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 81
ID ADB91646 standard; protein, 399 AA.
DE Human secreted protein #SEQ ID 592.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 7; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 82
ID ADC74298 standard; protein, 399 AA.
DE Human secreted protein - SEQ ID 931.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1688; DB 7; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 83
ID ADL77755 standard; protein, 399 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1237.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
Query Match 100.0%; Score 1688; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 84
ID ADL77754 standard; protein, 399 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1236.

PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 100.0%; Score 1688; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 85
ID ADL67172 standard; protein; 399 AA.
DE Human B7-H6 protein SEQ ID NO:42.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 100.0%; Score 1688; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 86
ID ADN3531 standard; protein; 399 AA.
DE Human STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
RESULT 87
ID AAM33874 standard; protein; 399 AA.
DE Human polypeptide; SEQ ID NO: 3986.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.5%; Score 1680; DB 4; Length 399;
Best Local Similarity 99.4%; Pred. No. 5.8e-135;
RESULT 88
ID ADL31953 standard; protein; 399 AA.
DE Human protein encoded by a full length cDNA clone seqid 3986.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 99.5%; Score 1680; DB 8; Length 399;
Best Local Similarity 99.4%; Pred. No. 5.8e-135;
RESULT 89
ID AAB04290 standard; protein; 386 AA.
DE Human gene 11 encoded secreted protein fragment, SEQ ID NO:154.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.3%; Score 1625; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.8e-130;
RESULT 90
ID ADL67174 standard; protein; 281 AA.
DE Human B7-H6 (ECD) protein SEQ ID NO:44.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 87.7%; Score 1480; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 4.6e-118;
RESULT 91
ID ADA57531 standard; protein; 305 AA.
DE Human secreted protein #466.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 92
ID ADA4415 standard; protein; 305 AA.
DE Human secreted protein.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 93
ID ABR46114 standard; protein; 305 AA.
DE Human secreted protein, SEQ ID 1005.

PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 94
ID ABR00282 standard; protein; 305 AA.
DE Human gene 147 encoded secreted protein HSDEK49, SEQ ID NO:571.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 6; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 95
ID ADB91804 standard; protein; 305 AA.
DE Human secreted protein #5EQ ID 750.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 7; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 96
ID ADC74547 standard; protein; 305 AA.
DE Human secreted protein - SEQ ID 1180.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 1137; DB 7; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 97
ID ADN35312 standard; protein; 305 AA.
DE Human short STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 67.4%; Score 1137; DB 8; Length 305;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 98
ID AAY30814 standard; protein; 306 AA.
DE Human secreted protein encoded from gene 4.
PN WO9940100-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.4%; Score 983; DB 2; Length 306;
Best Local Similarity 70.4%; Pred. No. 1.1e-88;
RESULT 99
ID AAM93588 standard; protein; 184 AA.
DE Human polypeptide; SEQ ID NO: 3387.
PN EP1396543-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 58.2%; Score 983; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
RESULT 100
ID ADL31354 standard; protein; 184 AA.
DE Human protein encoded by a full length cDNA clone seqid 3387.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 58.2%; Score 983; DB 8; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
RESULT 101
ID AAY82322 standard; protein; 175 AA.
DE Human protein transport molecule (PTM) SEQ ID NO:6.
PN WO200012703-A2.
PD 09-MAR-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 51.5%; Score 870; DB 3; Length 175;
Best Local Similarity 64.7%; Pred. No. 3.6e-66;
RESULT 102
ID ADK70486 standard; protein; 175 AA.
DE Respiratory disease differentially expressed protein #52.
PN WO2003101283-A2.

PD 11-DEC-2003.
PA (INCY-) INCTTE CORP.
Query Match 51.5%; Score 870; DB 8; Length 175;
Best Local Similarity 64.7%; Pred. No. 3.6e-66;
RESULT 103
ID ADL67144 standard; protein; 280 AA.
DE Mouse B7-H6 protein SEQ ID NO:14.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 43.1%; Score 728; DB 8; Length 280;
Best Local Similarity 47.0%; Pred. No. 9.6e-54;
RESULT 104
ID ADN35313 standard; protein; 280 AA.
DE Murine STGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 43.1%; Score 728; DB 8; Length 280;
Best Local Similarity 47.0%; Pred. No. 9.6e-54;
RESULT 105
ID ADL67146 standard; protein; 188 AA.
DE Mouse B7-H6(ECD) protein SEQ ID NO:16.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 36.3%; Score 613; DB 8; Length 188;
Best Local Similarity 45.7%; Pred. No. 3.8e-44;
RESULT 106
ID AAB10596 standard; protein; 93 AA.
DE Human macrophage-expressed protein #21.
PN WO200164839-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.1%; Score 492; DB 4; Length 93;
Best Local Similarity 98.9%; Pred. No. 3.3e-34;
RESULT 107
ID ADH80723 standard; protein; 300 AA.
DE Human polypeptide #40.
PN US200323054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match 10.7%; Score 180; DB 8; Length 300;
Best Local Similarity 27.9%; Pred. No. 7.8e-07;
RESULT 108
ID AAY23321 standard; protein; 299 AA.
DE Amino acid sequence of the PRO301 polypeptide.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 109
ID AAW74464 standard; protein; 299 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIX-) SMITHKLINE BEECHAM CORP.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 110
ID AAY08071 standard; protein; 299 AA.
DE Human PRO307 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 111
ID AAY13364 standard; protein; 299 AA.
DE Amino acid sequence of protein PRO301.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 112
ID AAY76011 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:189.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 113
ID AAY76076 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:331.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 114
ID AAY70670 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO20015797-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 115
ID AAB24405 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:90.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 116
ID AAY95344 standard; protein; 299 AA.
DE Human PRO301 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 117
ID AAB80232 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 118
ID AAW93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 119
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.

PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 120
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 121
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 122
ID AAU00823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 123
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 124
ID AAB53086 standard; protein; 299 AA.
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 125
ID AAU14405 standard; protein; 299 AA.
DE Human novel protein #276.
PN WO20015437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 126
ID AAU14404 standard; protein; 299 AA.
DE Human novel protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 127
ID AAU14168 standard; protein; 299 AA.
DE Human novel protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 128
ID AAB03896 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN WO200136440-A1.
PD 25-MAY-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 129
ID AAE03840 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HMCMA29, SEQ ID NO: 86.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 130
ID AAE03870 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HMCMA29, SEQ ID NO:116.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 131
ID ABB90290 standard; protein; 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 132
ID ABB84843 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 133
ID ABB64551 standard; protein; 299 AA.
DE Human albumin fusion protein #1226.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 134
ID ABB64552 standard; protein; 299 AA.
DE Human albumin fusion protein #1227.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 135
ID ABB72215 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 331.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 136
ID ABB72150 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 189.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 137
ID ABB95449 standard; protein; 299 AA.
DE Human angiogenesis related protein PRO301 SEQ ID NO: 54.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERR/) GERBER H.
PA (GERR/) GERITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARK/) MARSTERS S A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 138
ID ABU71610 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 139
ID ABO17798 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 140
ID ABU71465 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 141
ID ABO25173 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 142
ID ABU81052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003040311-A1.
PD 02-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 143
ID ABU71911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003030530-A1.
PD 02-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 144
ID ABO01194 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;

RESULT 145
ID ABU66752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 146
ID ABU54367 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 147
ID ABU67291 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 148
ID ABO47382 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 149
ID ABU59633 standard; protein; 299 AA.
DE Novel secreted and transmembrane protein PRO301.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 150
ID ABO25023 standard; protein; 299 AA.
DE Human secreted/transmembrane protein (PRO) #183.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 151
ID ABU64519 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #23.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 152
ID ABU72059 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 153
ID ABU67365 standard; protein; 299 AA.
DE Human secreted protein PRO301.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 154

ID ABU67160 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 155
ID ABO14885 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 156
ID ABU07736 standard; protein; 299 AA.
DE Human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 157
ID AAO16451 standard; protein; 299 AA.
DE Human junctional adhesion molecule 1 (hujAM1).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELLY) LILLY & CO ELI.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 158
ID ABU67028 standard; protein; 299 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 159
ID ABU69642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 160
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 161
ID ABO14824 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 162
ID ADA45885 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 163
ID ADA76316 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 164
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 165
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 166
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 167
ID ADB19374 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 168
ID ADB27915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 169
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 170
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 171
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 172
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.

PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 173
ID ABO32776 standard; protein: 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 174
ID ADA67539 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 175
ID ADB30546 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 176
ID ADA85442 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 177
ID ADA97054 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 178
ID ADA79358 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 179
ID ADA87497 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 180
ID ADB16699 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 181
ID ABO34636 standard; protein: 299 AA.
DE Human PRO polypeptide #21.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 182
ID ADA16155 standard; protein: 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003048621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 183
ID ADA91791 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 184
ID ADB14654 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 185
ID ADA47263 standard; protein: 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 186
ID ADB18615 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 187
ID ADA94030 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 188
ID ADB19926 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 189
ID ADB13238 standard; protein: 299 AA.
DE Human PRO polypeptide #183.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 190
ID ABO43331 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003044945-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 191
ID ADA74492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 192
ID ADA42300 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 193
ID ADB24725 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 194
ID ADA82249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 195
ID ADA75212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 196
ID ADA85290 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 197
ID ADA84738 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 198
ID ABO17514 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 199
ID ADB23994 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 200
ID ADA80522 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 201
ID ADA75764 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 202
ID ADA46989 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 203
ID ADB25285 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 204
ID ADA93461 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 205
ID ADB26811 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030932147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 206
ID ADB31098 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 207
ID ADA61026 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 208
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 209
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;

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Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 209
ID ADA96502 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 210
ID ADA81074 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 211
ID ADA95950 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 212
ID ADB26259 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 213
ID ADB2144 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 214
ID ADA77523 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 215
ID ADB18263 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 216
ID ADA86946 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 217
ID ADA16579 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 218
ID ADA13008 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 219
ID ADA41876 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 220
ID ADA88049 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 221
ID ADA46437 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 222
ID ADA17223 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 223
ID ADA42726 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 224
ID ADB28467 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 225
ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 226
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 227
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ID ADA8601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 228
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 229
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 230
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 231
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 232
ID ABO17575 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 233
ID ADA66987 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 234
ID ADB22848 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 235
ID ADB23621 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 236
ID ADA93343 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082712-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 237
ID ADB15406 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 238
ID ADB3658 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 239
ID ADB38106 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 240
ID ADB66578 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 241
ID ADB89658 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082658-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 242
ID ADB90390 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 243
ID ADB77645 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 244
ID ADB39491 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 245
ID ADB74781 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082542-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 246				
ID ADB47114 standard; protein, 299 AA.				
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003082687-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 247				
ID ADB86721 standard; protein, 299 AA.				
DE Human PRO polypeptide #183.				
PN US2003082697-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 248				
ID ADB71326 standard; protein, 299 AA.				
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003082696-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 249				
ID ADB34483 standard; protein, 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077717-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 250				
ID ADB35587 standard; protein, 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077719-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 251				
ID ADB33931 standard; protein, 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077716-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 252				
ID ADB35035 standard; protein, 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077718-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 253				
ID ADB36139 standard; protein, 299 AA.				
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077720-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 254				
ID ADB46534 standard; protein, 299 AA.				
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003082692-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 255				
ID ADB46534 standard; protein, 299 AA.				
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003082692-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5;	DB 7;	Length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1e-06;		
RESULT 256				
ID ADB39627 standard; protein, 299 AA.				
DE Human secreted/transmembrane protein, #25.				

Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 264		
ID	ADCC3841 standard; protein; 299 AA.	
DE	Human secreted/transmembrane protein, #25.	
PN	US2003073077-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 265		
ID	ADCI2911 standard; protein; 299 AA.	
DE	Human secreted/transmembrane protein, #25.	
PN	US2003073079-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 266		
ID	ADCC5407 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003092106-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 267		
ID	ADCT1954 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003092107-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 268		
ID	ADCC5933 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003092105-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 269		
ID	ADCC2940 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein Seq ID366.	
PN	US2003087365-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 270		
ID	ADCC7294 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein Seq ID366.	
PN	US2003087366-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 271		
ID	ADCC6485 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003087367-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 272		
ID	ADCC0960 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003087361-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;
RESULT 273		
ID	ADCC0960 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003087361-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	10.6%;	Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%;	Pred. No. 1e-06;

RESULT 273	ID ADC65487 standard; protein; 299 AA.
DE Human PRO polypeptide #183.	
PN US2003087362-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 274	ID ADC54585 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.	
PN US2003087363-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 275	ID ADC53546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.	
PN US2003087364-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 276	ID ADC59069 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.	
PN US2003087359-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 277	ID ADC55947 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.	
PN US2003087360-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 278	ID ADC12363 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seg ID366.	
PN US2003087346-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 279	ID ADIC12363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.	
PN US2003082541-A1.	
PD 01-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 280	ID ADD03191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003092104-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 281	ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003087348-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 282	ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003087348-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;
RESULT 282	ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.	
PN US2003087348-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Query Match	10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity	26.5%; Pred. No. 1e-06;

ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 283
ID ADC48491 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 284
ID ADD10020 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 285
ID ADD04595 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 286
ID ADC80551 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 287
ID ADD11058 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 288
ID ADD10343 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 289
ID ADC47939 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 290
ID ADD04918 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 291
ID ADC79999 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 292
ID ADD11303 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 293
ID ADD09468 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 294
ID ADD03924 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 295
ID ADD03500 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 296
ID ADD41181 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 297
ID ADD52320 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 298
ID ADD53060 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 299
ID ADD53612 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 300
ID ADD37096 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.

PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 301
ID ADD51768 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 302
ID ADD02567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 303
ID ADD02001 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 304
ID ADD54183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 305
ID ADD92500 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 306
ID ADD91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 307
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 308
ID ADE33307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 309
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 310
ID ADD79463 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 311
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 312
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 313
ID ADD91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 314
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 315
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 316
ID ADD80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 317
ID ADD93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 318
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199025-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 319			
ID AD834752 standard; protein; 299 AA.			
DE Human secreted/cranmembrane protein, #25.			
PN US2003077583-A1.			
PD 24-APR-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 320			
ID AD818920 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199026-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 321			
ID AD843116 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199033-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 322			
ID AD895905 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199059-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 323			
ID AD822791 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199064-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 324			
ID AD878909 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003203429-A1.			
PD 30-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 325			
ID AD832859 standard; protein; 299 AA.			
DE Novel human secreted and transmembrane protein PRO301.			
PN US2003194766-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 326			
ID AD842551 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199032-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 327			
ID AD80567 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003207418-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 328			
ID AD895995 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199028-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 329			
ID AD840879 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199031-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 330			
ID AD804678 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003199034-A1.			
PD 23-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 331			
ID AD892807 standard; protein; 299 AA.			
DE Human PRO polypeptide #183.			
PN US2003194777-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 332			
ID AD821516 standard; protein; 299 AA.			
DE Novel human secreted and transmembrane protein PRO301.			
PN US2003207355-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.	10.6%;	Score 178.5; DB 7;	Length 299;
Query Match			
Best Local Similarity	26.5%;	Pred. No. 1e-06;	
RESULT 333			
ID AD823157 standard; protein;			

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Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 337
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 338
ID ADH62528 standard; protein; 299 AA.
DE Human PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 339
ID ADH59235 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 340
ID ADH55296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 341
ID ADH55848 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 342
ID ADI38014 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 343
ID ADI64067 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 344
ID ADI65016 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 345
ID ADI63515 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 346
ID ADH81929 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 347
ID ADH81377 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 348
ID ADJ26282 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 349
ID ADM82546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 350
ID ADN15945 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 351
ID ADN16574 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 352
ID ADN15393 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 353
ID ADN14841 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 354
ID ADC81103 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
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PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 355
ID ADE79197 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 356
ID ADE76551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 357
ID ADE87915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 358
ID ADE86319 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 359
ID ADE79621 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 360
ID ADE75767 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 361
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003128592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 362
ID ADE41304 standard; protein; 299 AA.
DE Human secreted/cranmembrane PRO polypeptide #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 363
ID ADE23343 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092108-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 364
ID ADE23895 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 365
ID ADE24538 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 366
ID ADE87363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 367
ID ADE89229 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 368
ID ADE41186 standard; protein; 299 AA.
DE Human secreted/cranmembrane polypeptide PRO301.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 369
ID ADE73832 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 370
ID ADE18368 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 371
ID ADE86677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 372
ID ADE93586 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003211576-A1.
PD 13-NOV-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 373
ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 374
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 375
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 376
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 377
ID ADF34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 378
ID ADE96505 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 379
ID ADE92255 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 380
ID ADE90556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 381
ID ADE91703 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 382
ID ADE96932 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 383
ID ADG40402 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODD/) GODOWSKI P. J.
PA (GURN/) GURNEY A. L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 384
ID ADF73796 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 385
ID ADG02282 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 386
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 387
ID ADG20138 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 388
ID ADF98044 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 389
ID ADG24261 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 390
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ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 391
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 392
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 393
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 394
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 395
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 396
ID ADF98615 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 397
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 398
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 399
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 400
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 401
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 402
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 403
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 404
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 405
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 406
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 407
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 408
ID ADF98615 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 409
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 410
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 411
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 412
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 413
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 414
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 415
ID ADG58555 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 416
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 417
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027146-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 418
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 419
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 420
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 421
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 422
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 423
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 424
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 425
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 426
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 427
ID ADG81108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 428
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 429
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 430
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 431
ID ADH28546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 432
ID ADG54691 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 433
ID ADG59731 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 434
ID ADH20431 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 435
ID ADH43487 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 436
ID ADH07286 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODDARD P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 437
ID ADH59631 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 438
ID ADH06859 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODDARD P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 439
ID ADH1155 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 440
ID ADH18601 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 441
ID ADH65321 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 442
ID ADH37584 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 443
ID ADG09898 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009546-A1.

PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 444
ID ADH97380 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 445
ID ADH15369 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 446
ID ADG09246 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 447
ID ADI65748 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 448
ID ADI14701 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 449
ID ADH60491 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODD/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 450
ID ADI18296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 451
ID ADJ9548 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;

Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 452
ID ADL08741 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 453
ID ADI47176 standard; protein; 299 AA.
DE Human JAM-1 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 454
ID ADM25082 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 455
ID ADK40844 standard; protein; 299 AA.
DE Human platelet F11 receptor #1.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UINY) UNIV NEW YORK STATE RES FOUND.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 456
ID ADJ63577 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 457
ID ADM29832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 458
ID ADL77818 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 459
ID ADL77819 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 460
ID ADJ77472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 461
ID ADM2832 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 462
ID ADM5594 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 463
ID ADJ3132 standard; protein; 299 AA.
DE Human protein encoded by a full length cDNA clone seqID 3365.
PN EP396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 464
ID ADM27730 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 465
ID ADI26800 standard; protein; 299 AA.
DE Human JAM1 protein SEQ ID NO:54.
PN WO2004022778-A1.
PD 18-MAR-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 466
ID ADM42454 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 467
ID ADO06154 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 468
ID ADN35284 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 469
ID ADN05140 standard; protein; 299 AA.
DE Antiporietic protein sequence #749.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;

Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 470
ID ADM28316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1e-06;
RESULT 471
ID ADE09073 standard; protein; 320 AA.
DE Novel protein-related contig polypeptide sequence #139.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 7; Length 320;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 472
ID ADJ67616 standard; protein; 335 AA.
DE Human ovarian specific polypeptide SEQ ID NO:330.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 10.6%; Score 178.5; DB 8; Length 335;
Best Local Similarity 26.5%; Pred. No. 1.2e-06;
RESULT 473
ID ADE08038 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 178.5; DB 7; Length 336;
Best Local Similarity 26.5%; Pred. No. 1.2e-06;
RESULT 474
ID AAW14146 standard; protein; 319 AA.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 10.5%; Score 177; DB 2; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 475
ID AAY33323 standard; protein; 319 AA.
DE Amino acid sequence of the A33 antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 177; DB 2; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 476
ID AAB5863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.5%; Score 177; DB 4; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 477
ID ADA10947 standard; protein; 319 AA.
DE Human cDNA differentially expressed in colon cancer #43 product.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LAISEK A W.
PA (JONE/) JONES D A.
Query Match 10.5%; Score 177; DB 6; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.5e-06;
RESULT 478
ID ADH62533 standard; protein; 319 AA.
DE Human A33 antigenic protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.

PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A. L.
PA (NAPI/) NAPIER M. A.
PA (TUMAS/) TUMAS D.
PA (WOOD/) WOOD W. I.
Query Match
Best Local Similarity 10.5%; Score 177; DB 7; Length 319;
Pred. No. 1.5e-06;
RESULT 479
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C217.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 10.5%; Score 177; DB 7; Length 319;
Pred. No. 1.5e-06;
RESULT 480
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
PN W02004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 177; DB 8; Length 319;
Pred. No. 1.5e-06;
RESULT 481
ID ABP62881 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
PN W0200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 10.5%; Score 177; DB 5; Length 336;
Pred. No. 1.6e-06;
RESULT 482
ID ADC78439 standard; protein; 299 AA.
DE Human PRO301 protein.
PN W0200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 176.5; DB 3; Length 299;
Pred. No. 1.6e-06;
RESULT 483
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 268;
Pred. No. 1.5e-06;
RESULT 484
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A. L.
PA (NAPI/) NAPIER M. A.
PA (TUMAS/) TUMAS D.
PA (WOOD/) WOOD W. I.
Query Match
Best Local Similarity 10.4%; Score 176; DB 7; Length 268;
Pred. No. 1.5e-06;
RESULT 485
ID AAY23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 270;
Pred. No. 1.5e-06;
RESULT 486
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN W09927098-A2.

PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 273;
Pred. No. 1.5e-06;
RESULT 487
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 176; DB 2; Length 273;
Pred. No. 1.5e-06;
RESULT 488
ID ADH62553 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A. L.
PA (NAPI/) NAPIER M. A.
PA (TUMAS/) TUMAS D.
PA (WOOD/) WOOD W. I.
Query Match
Best Local Similarity 10.4%; Score 176; DB 7; Length 273;
Pred. No. 1.5e-06;
RESULT 489
ID ADH80722 standard; protein; 301 AA.
DE Human polypeptide #39.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y. T.
PA (LIU/) LIU C.
PA (ASUNDI/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X. B.
PA (WANG/) WANG Z. W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOI/) CAO Y.
PA (DRMA/) DRMANAC R. T.
Query Match
Best Local Similarity 10.3%; Score 173.5; DB 8; Length 301;
Pred. No. 2.8e-06;
RESULT 490
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 10.2%; Score 172.5; DB 8; Length 316;
Pred. No. 3.7e-06;
RESULT 491
ID AAY23326 standard; protein; 260 AA.
DE An A33 related antigen sequence.
PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 260;
Pred. No. 5.1e-06;
RESULT 492
ID AAY08072 standard; protein; 260 AA.
DE Human DNA40628 protein.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 260;
Pred. No. 5.1e-06;
RESULT 493
ID ADH62550 standard; protein; 260 AA.
DE Human PRO301 protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.

PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 7; Length 260;
RESULT 494
ID AAY3328 standard; protein; 263 AA.
DE An A33 related antigen sequence.
PN MO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 263;
RESULT 495
ID AAY08074 standard; protein; 263 AA.
DE Human DNA0628 protein fragment #2.
PN MO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 2; Length 263;
RESULT 496
ID ADH62552 standard; protein; 263 AA.
DE Human PRO301 protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.0%; Score 169.5; DB 7; Length 263;
RESULT 497
ID AAW61379 standard; protein; 298 AA.
DE Human junctional adhesion molecule protein.
PN MO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 9.9%; Score 167; DB 2; Length 298;
RESULT 498
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN MO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 9.9%; Score 167; DB 2; Length 300;
RESULT 499
ID AAY3325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN MO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 167; DB 2; Length 300;
RESULT 500
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.

PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 9.9%; Score 167; DB 7; Length 300;
RESULT 501
ID ADK40853 standard; protein; 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN US6699688-B1.
PD 02-MAR-2004.
PA (UTNY) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 9.9%; Score 167; DB 8; Length 300;
RESULT 502
ID ADN35293 standard; protein; 300 AA.
DE Human JAM protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 167; DB 8; Length 300;
RESULT 503
ID ABB83928 standard; protein; 365 AA.
DE PCAR SEQ ID NO 4.
PN US2002059654-A1.
PD 16-MAY-2002.
PA (BUHL/) BUHLER T. A.
PA (GADI/) GADIENT R A.
PA (KORN/) KORN R.
PA (MOVV/) MOVVA R.
Query Match
Best Local Similarity 9.8%; Score 166; DB 5; Length 365;
RESULT 504
ID ABB83927 standard; protein; 261 AA.
DE C-terminally truncated PCAR SEQ ID NO 2.
PN US2002059654-A1.
PD 16-MAY-2002.
PA (BUHL/) BUHLER T. A.
PA (GADI/) GADIENT R A.
PA (KORN/) KORN R.
PA (MOVV/) MOVVA R.
Query Match
Best Local Similarity 9.7%; Score 163.5; DB 5; Length 261;
RESULT 505
ID AAM14158 standard; protein; 318 AA.
DE Mouse A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 9.6%; Score 162.5; DB 2; Length 318;
RESULT 506
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO2000056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 9.5%; Score 160; DB 3; Length 280;
RESULT 507
ID ADA50171 standard; protein; 412 AA.
DE Human CAR/mouse SCF fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 9.4%; Score 158.5; DB 6; Length 412;
RESULT 508
ID AAY72878 standard; protein; 352 AA.
DE Human PRO5723 protein encoded by DNA82361 cDNA clone.
PN WO200116319-A2.

PD 08-MAR-2001.
ID (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 4; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 509
ID AAB50930 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 4; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 510
ID AAB65294 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:505.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 4; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 511
ID AAB84956 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:280.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 5; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 512
ID AAB95562 standard; protein; 352 AA.
DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERB/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.4%; Score 158; DB 5; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 513
ID ABUS58109 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 514
ID ABUS9187 standard; protein; 352 AA.
DE Novel human secreted or transmembrane protein PRO5723.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 515
ID ABUS2699 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;

RESULT 516
ID ABUS6018 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 517
ID ABUS80846 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 518
ID ABO33812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 519
ID ABUS14000 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 520
ID ABUS7585 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 521
ID ABG74762 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2002192752-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 522
ID ABUS9334 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 523
ID ABO26031 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 524
ID ABUS82155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 525
ID ABUS9040 standard; protein; 352 AA.

DE Human secreted/transmembrane protein, #177.
PN US2002143961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 526
ID ABO92418 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 527
ID ABO59483 standard; protein; 352 AA.
DE Novel human secreted or transmembrane protein PRO3301.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 528
ID ABO92249 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 529
ID ABO10955 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 530
ID ABO81707 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 531
ID ABO88646 standard; protein; 352 AA.
DE Human secreted and transmembrane polypeptide PRO5723.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 532
ID ABO34160 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 533
ID ABO72335 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 534
ID ABO38016 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 535
ID ABO21702 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 536
ID ABO10489 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO5723.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 537
ID ABO18033 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 538
ID ABO28141 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 539
ID ABO94721 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 540
ID ABO38946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 541
ID ABO72463 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 542
ID ABO393067 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 543
ID ABO34358 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO 5723.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 6; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 544
ID ABO53246 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;

RESULT 545
ID ADA22628 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 546
ID ABO22616 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 547
ID ADA06794 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #141.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 548
ID ABU72165 standard; protein; 352 AA.
DE Human membrane bound receptor/protein PRO5723 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 549
ID ADA39487 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 550
ID ADB83706 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 551
ID ADB80812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 552
ID ADB7353 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 553
ID ADB96513 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 554
ID ADB78435 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 555
ID ADB85083 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 556
ID ADB78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 557
ID ADB87255 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 558
ID ADB84837 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 559
ID ADB83952 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 560
ID ADB73107 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 561
ID ADC57985 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 562
ID ADC55349 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 563
ID ADC12216 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 9.4%; Score 158; DB 7; Length 352;
Pred. No. 7.4e-05;
RESULT 564
ID ADC56638 standard; protein; 352 AA.

DE Human PRO polypeptide #141.
PN US200306375-A1.
PD 03-APR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 565
ID ADCL1683 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 566
ID ADC35945 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 567
ID ADC21935 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 568
ID ADC4966 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 569
ID ADC49165 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 570
ID ADC49682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 571
ID ADC47543 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 572
ID ADC14805 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 573
ID ADC47288 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 574
ID ADD08337 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 575
ID ADC82162 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 576
ID ADD07804 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 577
ID ADC78163 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 578
ID ADC82695 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 579
ID ADD06398 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 580
ID ADD10569 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 581
ID ADD08875 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 582
ID ADC77917 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 583
ID ADD07124 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.

[illegible]

Beet Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 593		
ID AD554874 standard; protein; 352 AA.		
DE Human PRO polypeptide #141.		
PN US2002132253-A1.		
PD 19-SEP-2002.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%	Pred. No. 7,4e-05;
RESULT 594		
ID AD50361 standard; protein; 352 AA.		
DE Human PRO polypeptide #108.		
PN US2003096970-A1.		
PD 22-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 595		
ID AD551372 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
PN US003105289-A1.		
PD 05-JUN-2003.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 596		
ID AD311893 standard; protein; 352 AA.		
DE Human secreted/transmembrane protein PRO5723.		
PN US2003068647-A1.		
PD 10-APR-2003.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 597		
ID AD327028 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
PN US2003087304-A1.		
PD 08-MAY-2003.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 598		
ID AD326495 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
PN US2003087305-A1.		
PD 08-MAY-2003.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 599		
ID AD367432 standard; protein; 352 AA.		
DE Human PRO5723 amino acid sequence SEQ ID NO:505.		
PN US2002198148-A1.		
PD 26-DEC-2002.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 600		
ID AD354085 standard; protein; 352 AA.		
DE Immune disease treatment/diagnosis related PRO5723.		
PN US2003082199-A1.		
PD 01-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 601		
ID AD135686 standard; protein; 352 AA.		
DE Human PRO polypeptide #141.		
PN US2003050457-A1.		
PD 13-MAR-2003.		
Query Match	9.4%;	Score 158; DB 7; Length 352;
Beet Local Similarity	23.3%;	Pred. No. 7,4e-05;
RESULT 602		
ID AD100179 standard; protein; 352 AA.		
DE Novel human secreted and transmembrane protein PRO5723.		
PN US2003049682-A1.		

PD 13-MAR-2003.
Query Match 9.4%; Score 158; DB 7; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 603
ID ADC48919 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 604
ID ADE21090 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 605
ID ADE05934 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 606
ID ADD75163 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 607
ID ADD75909 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 608
ID ADD85141 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 609
ID ADE20598 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 610
ID ADE20844 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 611
ID ADE39141 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 612
ID ADE05688 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 613
ID ADD73673 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 614
ID ADD78513 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 615
ID ADE41530 standard; protein: 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 616
ID ADE21336 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 617
ID ADD77451 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 618
ID ADE20598 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 619
ID ADD75663 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 620
ID ADD74179 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;

Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 621
ID ADD74425 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 622
ID ADD76155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 623
ID ADD85647 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 624
ID ADE05196 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 625
ID ADD75409 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 626
ID ADD76953 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 627
ID ADD86721 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 628
ID ADD78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 629
ID ADD77697 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;

RESULT 630
ID ADD77943 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 631
ID ADD85401 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 632
ID ADD73933 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 633
ID ADD74671 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 634
ID ADD77199 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 635
ID ADD85893 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 636
ID ADE05442 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 637
ID ADD74917 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 638
ID ADF35631 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 639
ID ADG11881 standard; protein; 352 AA.

DE Human PRO5723 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 640
ID ADG05729 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 641
ID ADG27283 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 642
ID ADG1346 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 643
ID ADG12125 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 644
ID ADP94682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 645
ID ADG06778 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 646
ID ADH39122 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 647
ID ADH19751 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 648
ID ADH21244 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 649
ID ADH20284 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 650
ID ADH43713 standard; protein; 352 AA.
DE Human PRO polypeptide #140.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 651
ID ADG34212 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 652
ID ADI33682 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 653
ID ADH69776 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 654
ID ADI29937 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 655
ID ADW27134 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 656
ID ADK83058 standard; protein; 352 AA.
DE Human PRO polypeptide #140.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 657
ID ADK6692 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2004044180-A1.
PD 04-MAR-2004.

PA (GETH) GENENTECH INC.
Query Match 9.4%; Score 158; DB 8; Length 352;
Best Local Similarity 23.3%; Pred. No. 7.4e-05;
RESULT 658
ID AAW69697 standard; protein; 365 AA.
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
PN WO9833819-A1.
PD 06-AUG-1998.
PA (UYNV) UNIV NEW YORK STATE.
Query Match 9.4%; Score 158; DB 2; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 659
ID AAW57212 standard; protein; 365 AA.
DE Human coxsackievirus and adenovirus receptor.
PN WO9811221-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARBEN CANCER INST INC.
Query Match 9.4%; Score 158; DB 2; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 660
ID AAB47270 standard; protein; 365 AA.
DE Human CAR.
PN US6245966-B1.
PD 12-JUN-2001.
PA (UYTB-) UNIV TECHNOLOGY CORP.
Query Match 9.4%; Score 158; DB 4; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 661
ID ABB08040 standard; protein; 365 AA.
DE Human coxsackie-adenovirus receptor (CAR).
PN WO200229072-A2.
PD 11-APR-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
Query Match 9.4%; Score 158; DB 5; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 662
ID ABJ37063 standard; protein; 365 AA.
DE Human breast cancer / ovarian cancer related protein #39.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNium PHARM INC.
Query Match 9.4%; Score 158; DB 6; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 663
ID ADB97544 standard; protein; 365 AA.
DE Human CAR wild-type protein.
PN WO2003070915-A2.
PD 28-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 9.4%; Score 158; DB 7; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 664
ID ADN95226 standard; protein; 365 AA.
DE Human BEC/LBC-related protein sequence SeqID148.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 9.4%; Score 158; DB 7; Length 365;
Best Local Similarity 23.3%; Pred. No. 7.8e-05;
RESULT 665
ID ABU12046 standard; protein; 505 AA.
DE Human NOV4a CGS9871-01 protein SEQ ID 12.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 158; DB 6; Length 505;
Best Local Similarity 23.3%; Pred. No. 0.00012;
RESULT 666
ID ADJ67617 standard; protein; 351 AA.
DE Human ovarian specific polypeptide SEQ ID NO:331.
PN WO2004013311-A2.

PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 9.3%; Score 157.5; DB 8; Length 351;
Best Local Similarity 23.0%; Pred. No. 8.1e-05;
RESULT 667
ID ADA50172 standard; protein; 493 AA.
DE Human CAR/mouse anti-CD34 antibody fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match 9.3%; Score 157.5; DB 6; Length 493;
Best Local Similarity 23.7%; Pred. No. 0.00013;
RESULT 668
ID AAW82729 standard; protein; 264 AA.
DE Adenovirus PACTSG2-SCAR protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 9.3%; Score 156.5; DB 2; Length 264;
Best Local Similarity 25.9%; Pred. No. 6.7e-05;
RESULT 669
ID AAW82730 standard; protein; 277 AA.
DE Adenovirus SCAR.RGD protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 9.3%; Score 156.5; DB 2; Length 277;
Best Local Similarity 25.9%; Pred. No. 7.2e-05;
RESULT 670
ID AAU83699 standard; protein; 290 AA.
DE Human PRO protein, Seq ID NO 216.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 156.5; DB 5; Length 290;
Best Local Similarity 25.9%; Pred. No. 7.7e-05;
RESULT 671
ID AAW82731 standard; protein; 397 AA.
DE Adenovirus PACSG2SCAR.slg chimeric protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 9.3%; Score 156.5; DB 2; Length 397;
Best Local Similarity 25.9%; Pred. No. 0.00012;
RESULT 672
ID ADA50170 standard; protein; 412 AA.
DE Human CAR/SCF fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match 9.3%; Score 156.5; DB 6; Length 412;
Best Local Similarity 25.9%; Pred. No. 0.00012;
RESULT 673
ID ABG02019 standard; protein; 737 AA.
DE Novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.2%; Score 156; DB 4; Length 737;
Best Local Similarity 24.3%; Pred. No. 0.0003;
RESULT 674
ID AAY41692 standard; protein; 373 AA.
DE Human PRO 363 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 2; Length 373;

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 675
ID AAB33430 standard; protein: 373 AA.
DE Human PRO363 protein UNQ318 SEQ ID NO:87.
PN WO20053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 3; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 676
ID AAB44248 standard; protein: 373 AA.
DE Human PRO363 (UNQ318) protein sequence SEQ ID NO:59.
PN WO20053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 3; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 677
ID AAB12365 standard; protein: 373 AA.
DE Human PRO363 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 678
ID AAB48146 standard; protein: 373 AA.
DE Human A236 variant 2 polypeptide.
PN WO20069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 679
ID AAB48108 standard; protein: 373 AA.
DE Human A236 polypeptide.
PN WO20069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 680
ID AAB65293 standard; protein: 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:503.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 4; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 681
ID AAB83656 standard; protein: 373 AA.
DE Human PRO protein, Seq ID No 130.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 682
ID AAB84848 standard; protein: 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:64.
PN WO20020690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 683
ID AAB26448 standard; protein: 373 AA.
DE Human A236 protein.
PN US2002055139-A1.
PD 03-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIGHT/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 684
ID AAB95454 standard; protein: 373 AA.
DE Human angiogenesis related protein PRO363 SEQ ID NO: 64.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M B.
PA (GODD/) GODDARD A.
PA (GODO/) GODOBSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.1%; Score 153.5; DB 5; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 685
ID AAB58108 standard; protein: 373 AA.
DE Human PRO polypeptide #140.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 686
ID AAB59186 standard; protein: 373 AA.
DE Novel human secreted or transmembrane protein PRO363.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 687
ID AAB82698 standard; protein: 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 688
ID ABO17609 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 689
ID ABO60617 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 690
ID ABO80803 standard; protein: 373 AA.
DE Human PRO polypeptide #65.

PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 691
ID ABO25194 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 692
ID ABO33769 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 693
ID ABU13999 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 694
ID ABU81063 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 695
ID ABU72200 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002129706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 696
ID ABU72584 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 697
ID ABU66763 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 698
ID ABU84880 standard; protein; 373 AA.
DE Human secreted and transmembrane polypeptide PRO363.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 699
ID ABU59844 standard; protein; 373 AA.
DE Novel secreted and transmembrane protein PRO363.
PN US2003017563-A1.

PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 700
ID ABU61078 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 701
ID ABU59333 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 702
ID ABO26030 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 703
ID ABO25034 standard; protein; 373 AA.
DE Human secreted/transmembrane protein (PRO) #194.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 704
ID ABU80347 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 705
ID ABU82112 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 706
ID ABU59039 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 707
ID ABU92417 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 708
ID ABU59482 standard; protein; 373 AA.
DE Novel human secreted or transmembrane protein PRO5723.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

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RESULT 709
ID ABU67039 standard; protein; 373 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 388.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 710
ID ABU92248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 711
ID ABU10954 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 712
ID ABU81706 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 713
ID ABU88645 standard; protein; 373 AA.
DE Human secreted and transmembrane polypeptide PRO363.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 714
ID ABO34159 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 715
ID ADA45907 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 716
ID ADA76338 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 717
ID ABU72292 standard; protein; 373 AA.
DE Human PRO363 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 718
ID ADA18988 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 719
ID ADA61611 standard; protein; 373 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 720
ID ADA19396 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 721
ID ADB27937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 722
ID ADA86416 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 723
ID ADB15980 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 724
ID ADA38014 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 725
ID ADA47766 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 726
ID ADA21700 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 727
ID ADA10487 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 728
ID ADA10487 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003059831-A1.
PD 27-MAR-2003.
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Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 728
ID ADA67561 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 729
ID ADB30568 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 730
ID ADA85864 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 731
ID ADA18031 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 732
ID ADA97076 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 733
ID ADA79380 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 734
ID ADA87519 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 735
ID ADB16721 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 736
ID ADA28139 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 737

ID ADA91813 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 738
ID ADB14876 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 739
ID ADA24598 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 740
ID ADB18837 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 741
ID ADA94052 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 742
ID ADB19948 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 743
ID ADB13260 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 744
ID ABO43342 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 745
ID ABO19649 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 6; Length 373;
RESULT 746
ID ADA12259 standard; protein; 373 AA.

	DE	Human secreted/transmembrane polypeptide PRO363.	
PN	US2003055216-A1.		
PD	20-MAR-2003		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 747			
ID	ADA94719 standard; protein; 373 AA.		
DE	Human secreted/transmembrane protein PRO363.		
PN	US2003059832-A1.		
PD	27-MAR-2003.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 748			
ID	ADA74514 standard; protein; 373 AA.		
DE	Human PRO polypeptide #194.		
PN	US2003068798-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 749			
ID	ADB24747 standard; protein; 373 AA.		
DE	Human PRO polypeptide SEQ ID NO 388.		
PN	US2003077713-A1.		
PD	24-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 750			
ID	ADA82271 standard; protein; 373 AA.		
DE	Human PRO polypeptide #194.		
PN	US2003082701-A1.		
PD	01-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 751			
ID	ADA75234 standard; protein; 373 AA.		
DE	Human PRO polypeptide #194.		
PN	US2003073216-A1.		
PD	17-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 752			
ID	ADA85312 standard; protein; 373 AA.		
DE	Novel human secreted and transmembrane protein PRO363.		
PN	US2003082695-A1.		
PD	01-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 753			
ID	ADA84760 standard; protein; 373 AA.		
DE	Novel human secreted and transmembrane protein PRO363.		
PN	US2003082708-A1.		
PD	01-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 754			
ID	ADB30016 standard; protein; 373 AA.		
DE	Human PRO polypeptide #194.		
PN	US2003073214-A1.		
PD	17-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	9.1%; Score 153.5; DB 6;	Length 373;	
Best Local Similarity	27.0%; Pred. No. 0.00019;		
RESULT 755			
ID	ADA80544 standard; protein; 373 AA.		
DE	Human PRO polypeptide #194.		
PN	US2003082761-A1.		
PD			

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 765
ID ADA61048 standard; protein; 373 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 766
ID ADB24195 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 767
ID ADA96524 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 768
ID ADA81096 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 769
ID ADA95972 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 770
ID ADB26281 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 771
ID ADB21766 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 772
ID ABO34315 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO 363.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 773
ID ABO19540 standard; protein; 373 AA.
DE Novel human secreted and transmembrane polypeptide #8.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 6; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 774

ID ADA77545 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 775
ID ADB18285 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 776
ID ADA89668 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 777
ID ADA88071 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 778
ID ADA46459 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 779
ID ADB28489 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 780
ID ADB29041 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 781
ID ABO53245 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 782
ID ADA76993 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 783
ID ADA22626 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.

PN US20030406473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 784
ID ADB8623 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073213-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 785
ID ADB97628 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 786
ID ADB27385 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 787
ID ADB22318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 788
ID ADB22615 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 789
ID ADB06792 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 790
ID ADB72122 standard; protein; 373 AA.
DE Human membrane bound receptor/protein PRO363 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 791
ID ADB39485 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 792
ID ADB67009 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 793
ID ADB2870 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 794
ID ADB23643 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 795
ID ADB92365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 796
ID ADB15428 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 797
ID ADB83620 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 798
ID ADB80726 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 799
ID ADB73267 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US200306968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 800
ID ADB38680 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 801
ID ADB96511 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 27.0%; Pred. No. 0.00019;
Length 373;
RESULT 802
ID ADB78349 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092889-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 803
ID ADB3128 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 804
ID ADB6660 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 805
ID ADB84997 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 806
ID ADB89680 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 807
ID ADB90412 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 808
ID ADB39513 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 809
ID ADB78103 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 810
ID ADB73565 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 811
ID ADB87169 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003088067-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 812
ID ADB84751 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 813
ID ADB47136 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 814
ID ADB83866 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 815
ID ADB86743 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 816
ID ADB73021 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 817
ID ADB76281 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 818
ID ADB77348 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 819
ID ADB34505 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 820
ID ADB35609 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.


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Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 821
ID ADB33953 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 822
ID ADB35057 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 823
ID ADB36161 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 824
ID ADB46556 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 825
ID ADC43707 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 826
ID ADC57983 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 827
ID ADC55347 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 828
ID ADC12214 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 829
ID ADC61467 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 830
ID ADC63431 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 831
ID ADC66531 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 832
ID ADC56636 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 833
ID ADC68655 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 834
ID ADC62715 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 835
ID ADC67780 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 836
ID ADC11681 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003058403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 837
ID ADC41100 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 838
ID ADC67155 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.0%; Score 153.5; DB 7; Length 373;
Pred. No. 0.00019;
RESULT 839
ID ADC62091 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003073624-A1.
PD 17-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 840
ID ADC36859 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 841
ID ADC41724 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 842
ID ADC21849 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 843
ID ADC59429 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 844
ID ADC71976 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 845
ID ADC59955 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 846
ID ADC49880 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 847
ID ADC49079 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 848
ID ADC49596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 849
ID ADC47457 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 850
ID ADC52962 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 851
ID ADC57316 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 852
ID ADC60507 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 853
ID ADC50982 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 854
ID ADC65509 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 855
ID ADC54607 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 856
ID ADC53568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 857
ID ADC59091 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 858
ID ADC59091 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 858
ID ADC55969 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 859
ID ADC58539 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 860
ID ADC14603 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 861
ID ADC47202 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 862
ID ADD08335 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 863
ID ADD03213 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 864
ID ADC90205 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 865
ID ADC82160 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 866
ID ADC69624 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 867
ID ADC48513 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003105011-A1.
PD 05-JUN-2003.

PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 868
ID ADD10042 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 869
ID ADD07602 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 870
ID ADC78077 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 871
ID ADD04617 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 872
ID ADC82693 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 873
ID ADD06312 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 874
ID ADC80573 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 875
ID ADD11080 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 876
ID ADD10353 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105011-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 877
ID ADC47961 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 878
ID ADD08873 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 879
ID ADC77831 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 880
ID ADC80021 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 881
ID ADD07122 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 882
ID ADD11313 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 883
ID ADD09490 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 884
ID ADC83369 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 885
ID ADD50794 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

RESULT 886
ID ADD41203 standard; protein; 373 AA.
DE Human secreted and transmembrane protein PRO363.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 887
ID ADD52342 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 888
ID ADD51040 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 889
ID ADD53082 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 890
ID ADD5634 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 891
ID ADD55476 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 892
ID ADD37106 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 893
ID ADD56434 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 894
ID ADD51790 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 895
ID ADD02589 standard; protein; 373 AA.
DE Human PRO polypeptide #194.

PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 896
ID ADE050521 standard; protein, 373 AA.
DE Human PRO polypeptide #65.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 897
ID ADE02023 standard; protein, 373 AA.
DE Human PRO polypeptide #194.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 898
ID ADE54405 standard; protein, 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 899
ID ADE54872 standard; protein, 373 AA.
DE Human PRO polypeptide #140.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 900
ID ADE50275 standard; protein, 373 AA.
DE Human PRO polypeptide #65.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 901
ID ADE51286 standard; protein, 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 902
ID ADE49093 standard; protein, 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 903
ID ADE92522 standard; protein, 373 AA.
DE Human PRO polypeptide #194.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 904
ID ADE91418 standard; protein, 373 AA.
DE Human PRO polypeptide #194.
PN US2003199055-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 905
ID ADE04032 standard; protein, 373 AA.
DE Human PRO polypeptide #194.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 906
ID ADE31891 standard; protein, 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 907
ID ADE27026 standard; protein, 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 908
ID ADE32329 standard; protein, 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 909
ID ADE22261 standard; protein, 373 AA.
DE Human PRO polypeptide #194.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 910
ID ADE79485 standard; protein, 373 AA.
DE Human PRO polypeptide #194.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 911
ID ADE35147 standard; protein, 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 912
ID ADE16261 standard; protein, 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 913
ID ADE72876 standard; protein, 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 914
ID ADE4021 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 915
ID ADE17838 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 916
ID ADD91970 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 917
ID ADE33433 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 918
ID ADE33985 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 919
ID ADD80037 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 920
ID ADD93074 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 921
ID ADD72234 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 922
ID ADE19494 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

RESULT 923
ID ADE18942 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 924
ID ADE4138 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 925
ID ADD95927 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 926
ID ADE22813 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 927
ID ADD78931 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 928
ID ADE26493 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 929
ID ADE32881 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 930
ID ADE42573 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 931
ID ADE16885 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 932
ID ADD80589 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 933.
ID ADD89617 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 934.
ID ADE40901 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 935.
ID ADE04700 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 936.
ID ADE92829 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 937.
ID ADP46899 standard; protein: 373 AA.
DE Human secreted/cranemembrane protein, PRO363.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 938.
ID ADP67430 standard; protein: 373 AA.
DE Human PRO363 amino acid sequence SEQ ID NO:503.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 939.
ID ADG21538 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 940.
ID ADD23179 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 941.
ID ADP97514 standard; protein: 373 AA.
DE Human PRO polypeptide #194.

PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 942.
ID ADG80578 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 943.
ID ADG52656 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 944.
ID ADG59976 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 945.
ID ADG80026 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 946.
ID ADH5318 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 947.
ID ADH5870 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 948.
ID ADI35684 standard; protein: 373 AA.
DE Human PRO polypeptide #140.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 949.
ID ADI60736 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 7; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 950.
ID ADI64089 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207385-A1.
PD 06-NOV-2003.

PA	(GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 7;	Length 373;
Query Match					
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 951					
ID	AD165038 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207386-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 952					
ID	AD153537 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207387-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 953					
ID	ADH81951 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207388-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 954					
ID	AD100177 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003049682-A1.				
PD	13-MAR-2003.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 955					
ID	ADH81399 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207377-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 956					
ID	ADWM2568 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003087355-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 957					
ID	ADN15967 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003087353-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 958					
ID	ADN16596 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003087385-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
RESULT 959					
ID	ADN15415 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003087356-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Best Local Similarity		27.0%;	Pred. No. 0.00019;		
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;
Query Match		9.1%;	Score 153.5;	DB 7;	Length 373;

Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 960		
ID	ADN14863 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003087357-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 7; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 961		
ID	ADN48833 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003092888-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 962		
ID	ADN81125 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003092115-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 963		
ID	ADN21004 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003100735-A1.	
PD	29-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 964		
ID	ADN05848 standard; protein; 373 AA.	
DE	Human PRO polypeptide #65.	
PN	US2003100728-A1.	
PD	29-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 965		
ID	ADN76573 standard; protein; 373 AA.	
DE	Human PRO polypeptide #194.	
PN	US2003100087-A1.	
PD	29-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 966		
ID	ADD75077 standard; protein; 373 AA.	
DE	Human PRO polypeptide #65.	
PN	US2003100712-A1.	
PD	29-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 967		
ID	ADD75823 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003100717-A1.	
PD	29-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 968		
ID	ADD85055 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003100722-A1.	
PD	29-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;
RESULT 969		
ID	ADD85055 standard; protein; 373 AA.	
DE	Novel human secreted and transmembrane protein PRO363.	
PN	US2003100722-A1.	
PD	29-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	9.1%;	Score 153.5; DB 8; Length 373;
Best Local Similarity	27.0%;	Pred. No. 0.00019;

RESULT 969
ID ADD86881 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 970
ID ADE20758 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 971
ID ADE39055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 972
ID ADD87937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 973
ID ADD86341 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 974
ID ADE05602 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 975
ID ADD73587 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 976
ID ADE75789 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 977
ID ADE48393 standard; protein; 373 AA.
DE Human secreted/transmembrane protein. PRO363.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 978

ID ADD76427 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 979
ID ADE41314 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 980
ID ADE23365 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 981
ID ADE21250 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 982
ID ADD77365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 983
ID ADE20512 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 984
ID ADD75577 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 985
ID ADD74093 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 986
ID ADD74339 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 987
ID ADD76069 standard; protein; 373 AA.

DE Novel human secreted and transmembrane protein PRO363.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 988
ID ADD85561 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 989
ID ADE23917 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 990
ID ADE24560 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 991
ID ADD87385 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 992
ID ADE05110 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 993
ID ADD75323 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 994
ID ADD76867 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 995
ID ADD86635 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 996
ID ADE89251 standard; protein; 373 AA.
DE Human PRO polypeptide #194.

PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 997
ID ADD78103 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 998
ID ADE18390 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 999
ID ADE88699 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1000
ID ADE89494 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003130181-A1.
PD 10-UTL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERP/) GERRTSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUDS/) KUD S S.
PA (NAPJ/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1001
ID ADD77611 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1002
ID ADD77857 standard; protein; 373 AA.

DE Novel human secreted and transmembrane protein PRO363.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1003
ID ADD85315 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1004
ID ADD73647 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1005
ID ADD74585 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1006
ID ADD77113 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1007
ID ADD85607 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1008
ID ADD85356 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1009
ID ADD74631 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1010
ID ADD61134 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1011
ID ADF39826 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1012
ID ADF45622 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1013
ID ADE94719 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1014
ID ADE91130 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1015
ID ADF35629 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1016
ID ADE95271 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1017
ID ADE93381 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1018
ID ADF24018 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1019
ID ADF40450 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1020
ID ADF23394 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203402-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1021				
ID ADF33377 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003194780-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1022				
ID ADF34962 standard; protein, 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003199029-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1023				
ID ADF26844 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199436-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1024				
ID ADF27480 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199437-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1025				
ID ADE92277 standard; protein, 373 AA.				
DE Novel human secreted and transmembrane protein PRO363.				
PN US2003199051-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1026				
ID ADE90578 standard; protein, 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003199063-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1027				
ID ADF41074 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199435-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1028				
ID ADF32753 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003211091-A1.				
PD 13-NOV-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1029				
ID ADF25119 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003211092-A1.				
PD 13-NOV-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1030				
ID ADF22090 standard; protein, 373 AA.				
DE Novel human secreted and transmembrane protein PRO363.				
PN US2003207360-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1031				
ID ADF34009 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003194410-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1032				
ID ADF46246 standard; protein, 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003185344-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.	9.1%;	Score 153.5;	DB 8;	Length 373;
Query Match				
Best Local Similarity	27.0%;	Pred. No. 0.00019;		
RESULT 1033				
ID ADE91725 standard; protein, 373 AA.				
DE Novel human secreted and transmembrane protein PRO363.				
PN US2003199058-A1.				
PD 23-O				

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Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1039
ID ADG20160 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1040
ID ADF98066 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1041
ID ADG24283 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1042
ID ADF98637 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1043
ID ADG03468 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1044
ID ADF99189 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1045
ID ADG16774 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1046
ID ADG05233 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1047
ID ADG19500 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1048
ID ADG11260 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1049
ID ADG13337 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1050
ID ADG08394 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1051
ID ADG15564 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1052
ID ADG12039 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1053
ID ADF96962 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1054
ID ADG06147 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1055
ID ADG23731 standard; protein: 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1056
ID ADG04020 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1057
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ID ADG24921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1058
ID ADF94596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1059
ID ADG07218 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1060
ID ADG07770 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1061
ID ADG06692 standard; protein; 373 AA.
DE Human pro polypeptide #65.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1062
ID ADG55265 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1063
ID ADG60929 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1064
ID ADG62033 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1065
ID ADG82234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1066
ID ADG57473 standard; protein; 373 AA.

DE Novel human secreted and transmembrane protein PRO363.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1067
ID ADG56921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1068
ID ADG55817 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1069
ID ADG58577 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1070
ID ADG70943 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1071
ID ADH39036 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1072
ID ADG58025 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1073
ID ADG53609 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1074
ID ADG71495 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1075
ID ADG50232 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.

Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1094
ID ADG59753 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1095
ID ADG50856 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1096
ID ADH43497 standard; protein; 373 AA.
DE Human PRO polypeptide #32.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1097
ID ADG58800 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1098
ID ADG34126 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1099
ID ADG62256 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1100
ID ADI181177 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1101
ID ADI33596 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1102
ID ADH69690 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;

RESULT 1103
ID ADH25281 standard; protein; 373 AA.
DE Human neurotrophin homologue related protein sequence SRQ ID NO:59.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1104
ID ADG09920 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1105
ID ADI15391 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1106
ID ADG09268 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1107
ID ADI14723 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1108
ID ADI29851 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1109
ID ADI18318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1110
ID ADM27248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US200404179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1111
ID ADJ63599 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1112

ID ADJ77494 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1113
ID ADK82842 standard; protein: 373 AA.
DE Human PRO polypeptide #32.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1114
ID ADK66606 standard; protein: 373 AA.
DE Human PRO polypeptide #65.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1115
ID ADJ65616 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1116
ID ADM27752 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1117
ID ADM17058 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1118
ID ADJ06892 standard; protein: 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1119
ID ADM42476 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1120
ID ADN05373 standard; protein: 373 AA.
DE Antiposioratic protein sequence #858.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1121
ID ADM28338 standard; protein: 373 AA.
DE Human PRO polypeptide #194.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1122
ID ADO36720 standard; protein: 373 AA.
DE Human UKW polypeptide, SEQ ID NO:2.
PN EP1416279-A1.
PD 06-MAY-2004.
PA (HOPF) HOPFMAN LA ROCHE & CO AG F.
Query Match 9.1%; Score 153.5; DB 8; Length 373;
Best Local Similarity 27.0%; Pred. No. 0.00019;
RESULT 1123
ID ADA54925 standard; protein: 512 AA.
DE Human protein, SEQ ID 2493.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.1%; Score 153.5; DB 6; Length 512;
Best Local Similarity 25.2%; Pred. No. 0.0003;
RESULT 1124
ID AAY53666 standard; protein: 4412 AA.
DE Sequence gi/1017427/emb/CAA62189 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 9.1%; Score 153.5; DB 3; Length 4412;
Best Local Similarity 22.0%; Pred. No. 0.0055;
RESULT 1125
ID ABB60991 standard; protein: 5635 AA.
DE Novel human protein, SEQ ID 78.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (GLAX) GLAXO GROUP LTD.
Query Match 9.1%; Score 153.5; DB 5; Length 5635;
Best Local Similarity 25.2%; Pred. No. 0.0077;
RESULT 1126
ID ADJ70089 standard; protein: 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1895.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 9.1%; Score 153.5; DB 7; Length 5636;
Best Local Similarity 25.2%; Pred. No. 0.0077;
RESULT 1127
ID ADJ83137 standard; protein: 5636 AA.
DE Human hemiscitin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRUSEN B D.
PA (PATR/) PATTURAJAN M.
PA (LEPL/) LEPLLEY D M.
PA (BURG/) BURGESS C B.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSER W M.
PA (SZEK/) SZEKERS E S.
PA (VERN/) VERNET C A M.
PA (LITL/) LI L.
PA (CASH/) CASHMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.

PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 7; Length 5636;
RESULT 1128
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 5636;
RESULT 1129
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 5636;
RESULT 1130
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match
Best Local Similarity 9.1%; Score 153.5; DB 8; Length 5636;
RESULT 1131
ID ADA50158 standard; protein; 393 AA.
DE Human CAR/mouse SCF mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 9.1%; Score 153; DB 6; Length 393;
RESULT 1132
ID ABG74786 standard; protein; 31267 AA.
DE Human RGS11 protein.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE/) TAKEIDA CHEM IND LTD.
Query Match
Best Local Similarity 9.1%; Score 153; DB 6; Length 31267;
RESULT 1133
ID ADA50159 standard; protein; 474 AA.
DE Human CAR/mouse anti-CD34 antibody mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 9.0%; Score 152; DB 6; Length 474;
RESULT 1134
ID AAB48145 standard; protein; 373 AA.
DE Human A236 variant 1 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match
Best Local Similarity 9.0%; Score 151.5; DB 4; Length 373;
RESULT 1135
ID AAU17996 standard; protein; 301 AA.
DE Human immunoglobulin polypeptide SEQ ID No 141.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 4; Length 301;
RESULT 1136
ID ABB10232 standard; protein; 301 AA.
DE Human CDNA SEQ ID NO: 540.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 4; Length 301;
RESULT 1137
ID ABP66819 standard; protein; 301 AA.
DE Human polypeptide SEQ ID NO 540.
PN US2002090872-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 8.9%; Score 151; DB 5; Length 301;
RESULT 1138
ID ADB31620 standard; protein; 301 AA.
DE Human novel protein SEQ ID NO 141.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 7; Length 301;
RESULT 1139
ID ADA50157 standard; protein; 393 AA.
DE Human CAR/SCF mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 8.9%; Score 151; DB 6; Length 393;
RESULT 1140
ID ABG02117 standard; protein; 434 AA.
DE Novel human diagnostic protein #2108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.9%; Score 151; DB 4; Length 434;
RESULT 1141
ID ABU62399 standard; protein; 466 AA.
DE Chimeric CAR/Hg/Pro-A gene product.
PN US6524572-B1.
PD 25-FEB-2003.
PA (RAIN-) RAINBOW THERAPEUTIC CO.
Query Match
Best Local Similarity 8.9%; Score 151; DB 6; Length 466;
RESULT 1142
ID AAB48147 standard; protein; 373 AA.
DE Human A236 variant 3 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 8.9%; Score 150.5; DB 4; Length 373;
RESULT 1143
ID ABG31321 standard; protein; 2652 AA.

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DE Predicted human adlcan-2 protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 8.7%; Score 147.5; DB 5; Length 2652;
Best Local Similarity 21.8%; Pred. No. 0.009;
ID ADL02250 standard; protein; 2652 AA.
DE Human OCP protein #6.
PN US200405301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 8.7%; Score 147.5; DB 8; Length 2652;
Best Local Similarity 21.8%; Pred. No. 0.009;
ID ABB70049 standard; protein; 2845 AA.
DE Human NOV1A.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.7%; Score 147.5; DB 5; Length 2845;
Best Local Similarity 21.8%; Pred. No. 0.0099;
ID ABB22401 standard; protein; 361 AA.
DE Novel human diagnostic protein #22392.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 146.5; DB 4; Length 361;
Best Local Similarity 24.5%; Pred. No. 0.00074;
ID ABB85862 standard; protein; 373 AA.
DE Murine adipocytes-derived protein.
PN WO20016720-A1.
PD 13-SEP-2001.
PA (KITA/) KITAMURA T.
PA (TSUR/) TSURUGA H.
Query Match 8.7%; Score 146.5; DB 4; Length 373;
Best Local Similarity 25.9%; Pred. No. 0.00077;
ID AAB48126 standard; protein; 373 AA.
DE Mouse A236 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 145.5; DB 4; Length 373;
Best Local Similarity 25.9%; Pred. No. 0.00094;
ID AAB26449 standard; protein; 373 AA.
DE Mouse A236 protein.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANT/) PANT Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIGHT/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 8.6%; Score 145.5; DB 5; Length 373;
Best Local Similarity 25.9%; Pred. No. 0.00094;
ID ABB66424 standard; protein; 2016 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26064.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 8.6%; Score 145; DB 4; Length 2016;
Best Local Similarity 25.6%; Pred. No. 0.01;
ID AAB48149 standard; protein; 373 AA.
DE Mouse A236 variant 2 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 144.5; DB 4; Length 373;
Best Local Similarity 26.1%; Pred. No. 0.0011;
ID AAB48150 standard; protein; 373 AA.
DE Mouse A236 variant 3 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 144.5; DB 4; Length 373;
Best Local Similarity 25.6%; Pred. No. 0.0011;
ID AAB48148 standard; protein; 373 AA.
DE Mouse A236 variant 1 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.6%; Score 144.5; DB 4; Length 373;
Best Local Similarity 26.1%; Pred. No. 0.0011;
ID ABB63044 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15924.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 8.5%; Score 143.5; DB 4; Length 467;
Best Local Similarity 22.1%; Pred. No. 0.0019;
ID ABB63041 standard; protein; 396 AA.
DE Murine neccin-like protein 1.
PN WO2003064992-A2.
PD 07-AUG-2003.
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PA (LARR/) LARRICK J W.
PA (WYCO/) WYCOFF K L.
Query Match 8.4%; Score 142.5; DB 7; Length 396;
Best Local Similarity 19.6%; Pred. No. 0.0018;
ID AAB69287 standard; protein; 398 AA.
DE Amino acid sequence of long extracellular form of murine B7-1 (CD80).
PN WO200008057-A2.
PD 17-FEB-2000.
PA (IMMV ) IMMUNEX CORP.
Query Match 8.4%; Score 142.5; DB 3; Length 398;
Best Local Similarity 19.6%; Pred. No. 0.0019;
ID AAB00868 standard; protein; 404 AA.
DE Mouse brain immunoglobulin superfamily receptor (Bigr) protein.
PN WO200129083-A1.
PD 26-APR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 8.4%; Score 142.5; DB 4; Length 404;
Best Local Similarity 19.6%; Pred. No. 0.0019;
ID ABB68257 standard; protein; 1395 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 8.4%; Score 142.5; DB 4; Length 1395;
Best Local Similarity 21.1%; Pred. No. 0.01;
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RESULT 1160
ID ADE08000 standard; protein; 376 AA.
DE Novel protein (useful for identifying genetic disorders) #155.
PN W02003056152-A2.
PD 03-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.4%; Score 141.5; DB 7; Length 376;
Best Local Similarity 25.4%; Pred. No. 0.0021;
RESULT 1161
ID AAY13563 standard; protein; 1395 AA.
DE Drosophila Robo 1 polypeptide.
PN W09925833-A1.
PD 27-MAY-1999.
PA (REGC-) UNIV CALIFORNIA.
Query Match 8.4%; Score 141.5; DB 2; Length 1395;
Best Local Similarity 21.3%; Pred. No. 0.012;
RESULT 1162
ID AAY08401 standard; protein; 1395 AA.
DE Drosophila sp. ROBO1 protein.
PN W09920764-A1.
PD 29-APR-1999.
PA (REGC-) UNIV CALIFORNIA.
Query Match 8.4%; Score 141.5; DB 2; Length 1395;
Best Local Similarity 21.3%; Pred. No. 0.012;
RESULT 1163
ID ADB85335 standard; protein; 1395 AA.
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.
PN US0003170727-A1.
PD 11-SEP-2003.
PA (GOOD/) GOODMAN C S.
PA (KIDD/) KIDD T.
PA (BROS/) BROSE K.
PA (TESS/) TESSIER-LAVIGNE M.
Query Match 8.4%; Score 141.5; DB 7; Length 1395;
Best Local Similarity 21.3%; Pred. No. 0.012;
RESULT 1164
ID ABB71502 standard; protein; 1052 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41298.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 8.4%; Score 141; DB 4; Length 1052;
Best Local Similarity 25.1%; Pred. No. 0.0093;
RESULT 1165
ID AAM69698 standard; protein; 352 AA.
DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCR protein.
PN W09833819-A1.
PD 06-AUG-1998.
PA (UYNY-) UNIV NEW YORK STATE.
Query Match 8.3%; Score 140.5; DB 2; Length 352;
Best Local Similarity 25.4%; Pred. No. 0.0023;
RESULT 1166
ID AAM57213 standard; protein; 376 AA.
DE Mouse coxsackievirus and adenovirus receptor.
PN W09811221-A2.
PD 19-MAR-1998.
PA (DAND-) DANA PARBER CANCER INST INC.
Query Match 8.3%; Score 140.5; DB 2; Length 376;
Best Local Similarity 25.4%; Pred. No. 0.0025;
RESULT 1167
ID ADP56685 standard; protein; 265 AA.
DE Human junction adhesion molecule 3 splice variant 2 (hujAM3sv2) protein.
PN W02004053058-A2.
PD 24-JUN-2004.
PA (ELIL-) LILLY & CO ELI.
Query Match 8.3%; Score 139.5; DB 8; Length 265;
Best Local Similarity 24.0%; Pred. No. 0.0019;
RESULT 1168
ID AAY96294 standard; protein; 310 AA.
DE Human IGFAM-6 immunoglobulin.
PN W0200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.

Query Match 8.3%; Score 139.5; DB 3; Length 310;
Best Local Similarity 22.0%; Pred. No. 0.0024;
RESULT 1169
ID ADP56683 standard; protein; 310 AA.
DE Human junction adhesion molecule 3 (hujAM3) full-length protein.
PN W02004053058-A2.
PD 24-JUN-2004.
PA (ELIL-) LILLY & CO ELI.
Query Match 8.3%; Score 139.5; DB 8; Length 310;
Best Local Similarity 22.0%; Pred. No. 0.0024;
RESULT 1170
ID AAY96735 standard; protein; 310 AA.
DE PRO168, an A33 antigen homologue.
PN W0200036102-A2.
PD 22-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1171
ID AAB33457 standard; protein; 310 AA.
DE Human PRO168 protein UNQ859 SEQ ID NO:193.
PN W0200053758-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1172
ID AAB27276 standard; protein; 310 AA.
DE Human confuency regulated adhesion molecule 1 #2.
PN W0200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMP DICTAGENE SA.
Query Match 8.2%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1173
ID AAB80272 standard; protein; 310 AA.
DE Human PRO168 protein.
PN W0200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1174
ID AAM93905 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 2845.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELT-) HELIX RES INST.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1175
ID AAM93323 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 2845.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELT-) HELIX RES INST.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1176
ID AAU12440 standard; protein; 310 AA.
DE Human PRO168 polypeptide sequence.
PN W0200140466-A2.
PD 07-JUN-2001.
PA (GETH-) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1177
ID AAB80383 standard; protein; 310 AA.
DE Secreted protein encoded by gene #13.
PN W0200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1178
ID AAB80408 standard; protein; 310 AA.
DE Secreted protein encoded by gene #38.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1179
ID AAB80409 standard; protein; 310 AA.
DE Secreted protein encoded by gene #39.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1180
ID AAB92709 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2002098506-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1181
ID AAB91361 standard; protein; 310 AA.
DE Novel human secreted protein #7.
PN US2002098505-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1182
ID AAB84947 standard; protein; 310 AA.
DE Human PRO1868 protein sequence SEQ ID NO:262.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1183
ID AAB65297 standard; protein; 310 AA.
DE Human albumin fusion protein #1972.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1184
ID AAB65296 standard; protein; 310 AA.
DE Human albumin fusion protein #1971.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1185
ID AAB65298 standard; protein; 310 AA.
DE Human albumin fusion protein #1973.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1186
ID AAB31401 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PN US2002098507-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;

RESULT 1187
ID AAB95553 standard; protein; 310 AA.
DE Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PAMU/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.2%; Score 138.5; DB 5; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1188
ID AAB71650 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1189
ID AAB72377 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2002182618-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1190
ID AAB80867 standard; protein; 310 AA.
DE Human secreted and transmembrane polypeptide PRO1868.
PN US2002192668-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1191
ID ABO17684 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1192
ID AAB71505 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1193
ID ADA57610 standard; protein; 310 AA.
DE Human secreted protein #592.
PN WO2002102894-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1194
ID ADA57611 standard; protein; 310 AA.

DE Human secreted protein #592.
PN W02002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1195
ID ADA57309 standard; protein; 310 AA.
DE Human secreted protein #592.
PN W02002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1196
ID ABP7127 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (JAM3).
PN W02003006673-A2.
PD 23-JAN-2003.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1197
ID ABU81138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1198
ID ABU71951 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1199
ID ABO01834 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1200
ID ABU6838 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1201
ID ABU54407 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2002132240-A1.
PD 19-FEB-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1202
ID ABO47422 standard; protein; 310 AA.
DE Human secreted/transmembrane polypeptide PRO1868.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1203
ID ABG73314 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.

PN US2002164646-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1204
ID ABU59919 standard; protein; 310 AA.
DE Novel secreted and transmembrane protein PRO1868.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1205
ID ABO25109 standard; protein; 310 AA.
DE Human secreted/transmembrane protein (PRO) #269.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1206
ID ABU64559 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #63.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1207
ID ABU67405 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1208
ID ABO14925 standard; protein; 310 AA.
DE Human secreted / transmembrane polypeptide PRO1868.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1209
ID ABU60813 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160392-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1210
ID ABU67114 standard; protein; 310 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 538.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1211
ID ABU81236 standard; protein; 310 AA.
DE Human PRO1917polypeptide.
PN US2003032060-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1212
ID ABU69682 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868+H30.
PN US2003017463-A1.

PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1213
ID ABO14664 standard; protein; 310 AA.
DE Human secreted / transmembrane polypeptide PRO1868.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1214
ID ADA46057 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003023238-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1215
ID ADA76488 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1216
ID ADB29627 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1217
ID ADA19138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1218
ID ADA61761 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1219
ID ADB19546 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1220
ID ADB28087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1221
ID ADA86566 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082711-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1222
ID ADB16130 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1223
ID ADA47916 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1224
ID ADA18484 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1225
ID ABO32816 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1226
ID ADA67711 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1227
ID ADB30718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1228
ID ADA86014 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1229
ID ADA97226 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1230
ID ADA79530 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1231
ID ADA87669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1232
ID ADB16871 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1233
ID ABO34876 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1234
ID ADA16459 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1235
ID ADA91963 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1236
ID ADB15026 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1237
ID ADB16987 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1238
ID ADA94202 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1239
ID ADB20098 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
Query Match 8.2%; Score 138.5; DB 6; Length 310;

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1240
ID ADB13410 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1241
ID ABO43417 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1242
ID ADA74664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1243
ID ADA42604 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1244
ID ADB24897 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1245
ID ADA82421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1246
ID ADA75384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1247
ID ADA85462 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1248
ID ADA84910 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
Query Match 8.2%; Score 138.5; DB 6; Length 310;


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RESULT 1249
ID ABO17554 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1250
ID ADB30166 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1251
ID ADA80694 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1252
ID ADA75936 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1253
ID ADA47161 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1254
ID ADB25457 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1255
ID ADA93633 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1256
ID ADB26983 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1257
ID ADB31270 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1258
ID ADB16435 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003054447-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1259
ID ADA61198 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1260
ID ADB24345 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1261
ID ADA96674 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1262
ID ADA81246 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1263
ID ADA96122 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1264
ID ADB26431 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1265
ID ADB21916 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1266
ID ADA77695 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0029; Length 310;
RESULT 1267
ID ADB16435 standard; protein; 310 AA.
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DE Human PRO polypeptide #269.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1268
ID ADA67118 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1269
ID ADA16883 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1270
ID ADA13312 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1271
ID ADA42180 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1272
ID ADA88221 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1273
ID ADA46609 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1274
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1275
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1276
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.

PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1277
ID ADB29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1278
ID ABO01894 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003027256-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1279
ID ADA77143 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1280
ID ADA88773 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1281
ID ADA97778 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1282
ID ADB27535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1283
ID ADB22468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1284
ID ABO17615 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1285
ID ADA67159 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

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Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1286
ID ADB32020 standard; protein, 310 AA.
DE Human PRO polypeptide #269.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1287
ID ADB23793 standard; protein, 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1288
ID ADB92515 standard; protein, 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1289
ID ADB15578 standard; protein, 310 AA.
DE Human PRO polypeptide #269.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1290
ID ADB38830 standard; protein, 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1291
ID ADB38278 standard; protein, 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1292
ID ADB66750 standard; protein, 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1293
ID ADB89630 standard; protein, 310 AA.
DE Human PRO polypeptide #269.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1294
ID ADB90562 standard; protein, 310 AA.
DE Human PRO polypeptide #269.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1295
ID ADB77948 standard; protein, 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1296
ID ADB39663 standard; protein, 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1297
ID ADB75084 standard; protein, 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1298
ID ADB47286 standard; protein, 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1299
ID ADB86893 standard; protein, 310 AA.
DE Human PRO polypeptide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1300
ID ADB77498 standard; protein, 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1301
ID ADB34655 standard; protein, 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1302
ID ADB35759 standard; protein, 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1303
ID ADB34103 standard; protein, 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
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RESULT 1304
ID ADB35207 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1305
ID ADB36311 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1306
ID ADB46706 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1307
ID ADC28731 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1308
ID ADC39931 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1309
ID ADC40445 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1310
ID ADC19269 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1311
ID ADC34569 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1312
ID ADC29624 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1313

ID ADC29155 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1314
ID ADC41040 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1315
ID ADC19697 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1316
ID ADC34145 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1317
ID ADC13215 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1318
ID AAE38826 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003077657-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1319
ID ADC50579 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1320
ID ADC72126 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1321
ID ADC60105 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1322
ID ADC53112 standard; protein; 310 AA.

DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1323
ID ADC57466 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1324
ID ADC60657 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1325
ID ADC51132 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1326
ID ADC65659 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1327
ID ADC54757 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1328
ID ADC53718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1329
ID ADC59241 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1330
ID ADC56119 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1331
ID ADC58669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.

PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1332
ID ADC12667 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1333
ID ADC74383 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1016.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1334
ID ADC74606 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1239.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1335
ID ADC74607 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1240.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1336
ID ADD03363 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1337
ID ADC90355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1338
ID ADC69774 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1339
ID ADC48663 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1340
ID ADD10192 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194776-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1341
ID ADD04767 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1342
ID ADC080723 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1343
ID ADD11230 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1344
ID ADD10551 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1345
ID ADC4811 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1346
ID ADD05222 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1347
ID ADC80171 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1348
ID ADD1511 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1349
ID ADD09640 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1350
ID ADD04228 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1351
ID ADD03804 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1352
ID ADD41353 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1353
ID ADD52492 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1354
ID ADD53232 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1355
ID ADD53784 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1356
ID ADD37304 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1357
ID ADD51940 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1358
ID ADD02739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1359
ID ADD38106 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1360
ID ADD38009 standard; protein; 310 AA.
DE Human secreted protein #192.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1361
ID ADD38105 standard; protein; 310 AA.
DE Human secreted protein #288.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1362
ID ADD02173 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1363
ID ADD54355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1364
ID ADD92672 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1365
ID ADD91568 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1366
ID ADB04182 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1367
ID ADB32479 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1368
ID ADB22411 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1369
ID ADD79635 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1370
ID ADB42171 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1371
ID ADB17988 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1372
ID ADD92120 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1373
ID ADB33583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1374
ID ADB34135 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1375
ID ADB80187 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1376
ID ADD93224 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match      8.2% Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
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RESULT 1377
ID ADE19644 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1378
ID ADE35056 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1379
ID ADE19092 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1380
ID ADE43288 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1381
ID ADD96077 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1382
ID ADE22963 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1383
ID ADD79081 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003201429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1384
ID ADE33031 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1385
ID ADE42723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1386

ID ADD80739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1387
ID ADD89767 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1388
ID ADE41051 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1389
ID ADE04850 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1390
ID ADE92979 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1391
ID ADE21688 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1392
ID ADG23329 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1393
ID ADF97664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1394
ID ADG80728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1395
ID ADG80176 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1396
ID ADH62558 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A. L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1397
ID ADH59539 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1398
ID ADH55468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1399
ID ADH56020 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1400
ID ADI38318 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1401
ID ADI6439 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1402
ID ADI65188 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1403
ID ADI6387 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1404
ID ADH82101 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1405
ID ADH81549 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1406
ID ADI58518 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003170864-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1407
ID ADJ26586 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1408
ID ADM82718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1409
ID ADNI6117 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1410
ID ADNI6746 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1411
ID ADNI5565 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1412
ID ADNI5013 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.2%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1413
ID ADE81275 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1414
ID ADE79501 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1415
ID ADE76723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1416
ID ADE88087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1417
ID ADE86491 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1418
ID ADE79925 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1419
ID ADE75939 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1420
ID ADE73601 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1421
ID ADE841512 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1422
ID ADE23515 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1423
ID ADE24067 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1424
ID ADE24710 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1425
ID ADE87535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1426
ID ADE89401 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1427
ID ADE74136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1428
ID ADE18540 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1429
ID ADE88849 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1430
ID ADE99690 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;

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RESULT 1431
ID ADE94669 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1432
ID ADE91280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1433
ID ADE95421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1434
ID ADE93531 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1435
ID ADF35112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1436
ID ADE98809 standard; protein; 310 AA.
DE Human secreted/cranmembrane protein, #65.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1437
ID ADE92427 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1438
ID ADE90728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1439
ID ADE91675 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1440
ID ADE99236 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1441
ID ADG40706 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODR/) GODDARD P. J.
PA (GURN/) GURNEY A. L.
PA (MATH/) MATHER J. P.
PA (WILL/) WILLIAMS P. M.
PA (WOOD/) WOOD W. I.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1442
ID ADF74100 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1443
ID ADG02454 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1444
ID ADG22240 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1445
ID ADG20310 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1446
ID ADF98216 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1447
ID ADG24433 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1448
ID ADF98787 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003208055-A1.
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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1448
ID ADG03618 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1450
ID ADG99339 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1451
ID ADG16924 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1452
ID ADG05383 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1453
ID ADG19650 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1454
ID ADG73676 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1455
ID ADG13487 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1456
ID ADG08544 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1457
ID ADG15714 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003219885-A1.
PD 27-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1460
ID ADG23881 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1461
ID ADG04170 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1462
ID ADG25071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1463
ID ADG07368 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1464
ID ADG07920 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1465
ID ADG55415 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1466
ID ADG61079 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1467
ID A0662183 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1468
ID A0692519 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003207445-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1469
ID A0682384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1470
ID A0657623 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1471
ID A0657071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1472
ID A0655967 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1473
ID A0658727 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1474
ID A0671093 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1475
ID A0692946 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003207446-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1485

Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1476
ID A0658175 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1477
ID A0653759 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1478
ID A0671645 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1479
ID A0681832 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1480
ID A0630794 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1481
ID A0612161 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1482
ID A0652583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1483
ID A0654311 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1484
ID A0681280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1485

ID ADG56519 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1486
ID ADH12785 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1487
ID ADG61631 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1488
ID ADH28718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1489
ID ADG54863 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1490
ID ADG59903 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1491
ID ADH20735 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1492
ID ADH43695 standard; protein; 310 AA.
DE Human PRO polypeptide #131.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1493
ID ADH07590 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1494
ID ADH60135 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1495
ID ADH07163 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1496
ID ADH1337 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1497
ID ADH18905 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1498
ID ADI65625 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1499
ID ADI37884 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;
RESULT 1500
ID ADG10070 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 8.2%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0029;

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OM protein - protein search, using sw model

Run on: January 4, 2005, 06:06:41 ; Search time 116 Seconds
(without alignments)
1592.201 Million cell updates/sec

Title: US-10-767-374-2

Perfect score: 1688

Sequence: 1 MGILLGULLGLHGLTVDTYGR.....AYIMLCRKTSQEHVYEAAK 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 1500 summaries

Database :

1: uniprot_02:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	100.0	321	2	OGUX14
2	1688	100.0	321	2	AAQ88707
3	1688	100.0	399	2	O9Y279
4	728	43.1	280	2	O80WA3
5	728	43.1	280	2	BAC30780
6	178.5	10.6	299	1	JAM1_HUMAN
7	178.5	10.6	299	2	AAG28379
8	178.5	10.6	299	2	BAC11436
9	178.5	10.6	299	2	AAO84556
10	177	10.5	319	1	A33_HUMAN
11	177	10.5	319	2	AAH69705
12	177	10.5	319	2	AAH69723
13	177	10.5	319	2	AAH69745
14	177	10.5	319	2	AAH69761
15	177	10.5	319	2	AAH69789
16	172	10.2	7962	2	O10465
17	172	10.2	34350	2	O8W242
18	169.5	10.0	298	1	JAM1_BOVIN
19	169	10.0	365	2	O8WMT3
20	168	10.0	300	2	O8VCJ9
21	167	9.9	300	1	JAM1_MOUSE
22	167	9.9	300	2	O9JHY1
23	167	9.9	300	2	AAH65309
24	167	9.9	319	2	O9TUV9
25	166	9.8	319	1	O9TUB0
26	159.5	9.4	344	2	O9UKV4
27	158	9.4	344	2	OXUKV4
28	158	9.4	365	1	CVAR_HUMAN
29	157.5	9.3	332	2	O6P359
30	157.5	9.3	332	2	AAH64174
31	156.5	9.3	5516	2	O72248

32	156	9.2	289	2	O7ZW70	O7ZW70 xenopus lae
33	156	9.2	335	2	O9YGH1	O9YGH1 gallus gall
34	156	9.2	335	2	O9PWR4	O9PWR4 gallus gall
35	153.5	9.1	373	2	O9H6B4	O9H6B4 homo sapien
36	153.5	9.1	373	2	AAQ88706	AAQ88706 homo sapi
37	153.5	9.1	512	2	O96DN8	O96DN8 homo sapien
38	153.5	9.1	5636	2	O96RW7	O96RW7 homo sapien
39	151	8.9	390	2	O9H1X9	O9H1X9 homo sapien
40	149.5	8.9	344	2	O9R067	O9R067 ratius norv
41	149.5	8.9	358	2	O9R066	O9R066 ratius norv
42	146.5	8.7	373	2	O920S5	O920S5 mus musculu
43	145.5	8.6	335	2	O9YGV5	O9YGV5 gallus gall
44	145.5	8.6	332	2	O8KIG0	O8KIG0 ratius norv
45	145.5	8.6	373	2	O8R373	O8R373 mus musculu
46	145.5	8.6	1271	2	O6U714	O6U714 brachydantio
47	145.5	8.6	1271	2	AAQ85080	AAQ85080 brachydantio
48	145	8.6	3950	2	O7YRP5	O7YRP5 canis famli
49	144.5	8.5	537	2	O7PSJ8	O7PSJ8 anopheles g
50	143.5	8.5	403	2	O9VPO8	O9VPO8 drosophila
51	143.5	8.5	1052	1	FGR2_DROME	FGR2_DROME
52	143	8.5	448	2	O81GAS	O81GAS drosophila
53	142.5	8.4	372	2	O90Y50	O90Y50 brachydantio
54	142.5	8.4	396	2	O99N28	O99N28 m nectin-11
55	142.5	8.4	1395	2	O7KVK3	O7KVK3 drosophila
56	142.5	8.4	1395	2	AAFA6887	AAFA6887 drosophila
57	142.5	8.4	1429	2	O9W213	O9W213 drosophila
58	142.5	8.4	1429	2	AAW71113	AAW71113 drosophila
59	141.5	8.4	1395	2	O44924	O44924 drosophila
60	141	8.3	1052	2	O9VUC8	O9VUC8 drosophila
61	140.5	8.3	352	2	O91W66	O91W66 mus musculu
62	140.5	8.3	365	2	CVAR_MOUSE	P97792 mus musculu
63	140.5	8.3	365	2	O9DB58	O9DB58 mus musculu
64	140.5	8.3	397	2	O6XRC3	O6XRC3 homo sapien
65	140.5	8.3	397	2	AAPA7270	AAPA7270 homo sapi
66	140.5	8.3	4071	2	O6KD21	O6KD21 gallus gall
67	140.5	8.3	4071	2	CAES1322	CAES1322 gallus ga
68	140	8.3	1662	2	O7OIV4	O7OIV4 anopheles g
69	139.5	8.3	3410	2	O7TNO0	O7TNO0 ratius norv
70	139.5	8.3	3707	1	FGBM_MOUSE	O05793 mus musculu
71	139	8.2	377	2	O9VQY0	O9VQY0 drosophila
72	138.5	8.2	310	2	O9BX67	O9BX67 homo sapien
73	138.5	8.2	310	2	AAQ88701	AAQ88701 homo sapi
74	138.5	8.2	310	2	AAH12147	AAH12147 homo sapi
75	138.5	8.2	355	2	O8WMT8	O8WMT8 homo sapien
76	138.5	8.2	413	2	O6ZNT1	O6ZNT1 homo sapien
77	138.5	8.2	1323	2	BAD18394	BAD18394 gallus gall
78	138.5	8.2	4162	2	O80476	O80476 gallus gall
79	138.5	8.2	298	2	O98918	O80474 brachydantio
80	138	8.2	310	2	O9DB87	O9DB87 mus musculu
81	138	8.2	360	1	HEPL3_HUMAN	O96856 homo sapien
82	138	8.2	423	2	O8BU57	O8BU57 mus musculu
83	138	8.2	523	2	O80Z82	O80Z82 mus musculu
84	138	8.2	569	1	SILF_MOUSE	O92003 mus musculu
85	138	8.2	309	2	O96FT1	O96FT1 homo sapien
86	137.5	8.1	749	2	O967D9	O967D9 drosophila
87	137.5	8.1	902	2	O81Q17	O81Q17 drosophila
88	137.5	8.1	903	3	O9VOY1	O9VOY1 drosophila
89	137.5	8.1	903	3	O96VY8	O96VY8 drosophila
90	137.5	8.1	903	3	O96VY8	O96VY8 drosophila
91	137.5	8.1	1508	2	O6NR34	O6NR34 drosophila
92	137.5	8.1	1508	2	O9VOY2	O9VOY2 drosophila
93	137.5	8.1	1508	2	AAQ23565	AAQ23565 drosophila
94	137.5	8.1	1508	2	AAFS1029	AAFS1029 drosophila
95	137.5	8.1	1531	2	O967D7	O967D7 drosophila
96	137.5	8.1	2022	2	O7KQO5	O7KQO5 drosophila
97	137.5	8.1	2022	2	AAAS4901	AAAS4901 drosophila
98	137	8.1	310	2	O9PDM9	O9PDM9 mus musculu
99	137	8.1	310	2	O9PEK4	O9PEK4 m junctiona
100	137	8.1	359	1	LACH_DROME	O24372 drosophila
101	137	8.1	359	2	O9V6C2	O9V6C2 drosophila
102	137	8.1	1316	2	O7OB16	O7OB16 anopheles g
103	137	8.1	2016	2	O8MKW6	O8MKW6 drosophila
104	137	8.1	2016	2	O8MKW7	O8MKW7 drosophila

105	137	8.1	2016	2	Q9NBA1	Q9nba1 drosophila	178	129.5	7.7	1479	2	AAFS9040	AAFS9040 drosophila
106	137	8.1	2019	2	Q8MKM8	Q8mk8 drosophila	179	129.5	7.7	1482	2	Q9V4Y0	Q9v4y0 drosophila
107	137	8.1	2828	2	Q9NR99	Q9nr99 homo sapien	180	129.5	7.7	1375	1	UN52 CABEL	Q0652 caenorhabdi
108	136.5	8.1	330	2	P97269	P97269 cavia porce	181	129	7.6	308	2	Q8OWN3	Q8own3 mus musculu
109	136	8.1	283	2	Q9V776	Q9vc76 drosophila	182	129	7.6	324	2	Q77WM2	Q77wm2 mus musculu
110	136	8.1	584	2	Q9Y3Y8	Q9y3y8 homo sapien	183	129	7.6	343	2	Q8R4Y0	Q8r4y0 mus musculu
111	136	8.1	1827	2	Q9V6G5	Q9v6g5 drosophila	184	129	7.6	433	2	Q9V644	Q9v644 drosophila
112	136	8.1	1827	2	AAFS0456	AAFS0456 drosophila	185	129	7.6	1427	2	Q91562	Q91562 xenopus lae
113	135.5	8.0	298	2	Q8CSK9	Q8csk9 mus musculu	186	128.5	7.6	1040	2	Q6NZJ4	Q6nzj4 mus musculu
114	135	8.0	394	2	Q925F2	Q925f2 mus musculu	187	128.5	7.6	1040	2	AAH6106	AAH6106 mus muscu
115	135	8.0	838	2	Q90YML	Q90ym1 brachydanio	188	128.5	7.6	2053	2	Q81ZY4	Q81zy4 homo sapien
116	135	8.0	2013	2	Q9ERK8	Q9erch mus musculu	189	128	7.6	255	2	Q9VQ64	Q9vq64 drosophila
117	135	8.0	2013	2	Q8VHZ8	Q8vzh8 rattus norv	190	128	7.6	257	2	Q8R202	Q8r202 mus musculu
118	134.5	8.0	298	2	Q8CE95	Q8ce95 mus musculu	191	128	7.6	261	2	Q9D7L8	Q9d7l8 m mus muscu
119	134.5	8.0	303	2	Q7ZXR4	Q7zxr4 xenopus lae	192	128	7.6	261	2	AAH61082	AAH61082 mus muscu
120	134.5	8.0	450	2	Q6UX10	Q6ux10 homo sapien	193	128	7.6	343	2	Q8HYSA	Q8hy84 mus musculu
121	134.5	8.0	450	2	AAQ88711	AAq88711 homo sapi	194	128	7.6	344	2	Q9VYJ3	Q9vyj3 drosophila
122	134.5	8.0	2597	2	Q6WRH9	Q6wrh9 rattus norv	195	128	7.6	386	2	Q8B1N0	Q8b1n0 mus musculu
123	134.5	8.0	2597	2	AAQ16157	AAq16157 rattus no	196	128	7.6	392	2	Q7PSN2	Q7psn2 anopheles g
124	134	7.9	2217	2	Q8AV57	Q8av57 gallus gall	197	128	7.6	417	2	BAC29767	Bac29767 m 6 days
125	134	7.9	2623	2	Q6WR10	Q6wr10 homo sapien	198	128	7.6	977	2	Q96RD9	Q96rd9 homo sapien
126	134	7.9	2623	2	AAQ16156	AAq16156 homo sapi	199	127.5	7.6	299	2	Q7Q8F3	Q7q8f3 anopheles g
127	133.5	7.9	321	2	Q61NFO	Q61nf0 xenopus lae	200	127.5	7.6	1028	2	Q61NBS	Q61nb5 xenopus lae
128	133.5	7.9	321	2	AAH72333	AAh72333 xenopus 1	201	127.5	7.6	1028	2	AAH72368	AAh72368 xenopus 1
129	133.5	7.9	338	2	Q8N126	Q8n126 homo sapien	202	127.5	7.6	1340	2	Q8ND42	Q8nd42 homo sapien
130	133.5	7.9	398	2	AAQ88698	AAq88698 homo sapi	203	127.5	7.6	1306	1	XMLS CHICK	P11799 gallus gall
131	133.5	7.9	432	2	Q9UJPI	Q9ujp1 homo sapien	204	127.5	7.6	1906	1	AAQ35031	AAc29031 gallus ga
132	133.5	7.9	434	2	Q6DN72	Q6dn72 homo sapien	205	127	7.5	285	2	Q8BTK0	Q8btk0 mus musculu
133	133.5	7.9	484	2	Q26475	Q26475 schistocerc	206	127	7.5	337	1	OPCM CHICK	Q98892 gallus gall
134	133.5	7.9	487	2	Q7T2H2	Q7t2h2 gallus gall	207	127	7.5	344	1	Q9DP61	Q9d61 gallus gall
135	133.5	7.9	5175	2	Q810L3	Q810l3 caenorhabdi	208	127	7.5	632	2	Q6ZRK5	Q6zrk5 homo sapien
136	133.5	7.9	5198	2	Q76518	Q76518 caenorhabdi	209	127.5	7.5	632	2	BAC87305	Bac87305 homo sapi
137	133	7.9	305	2	Q8VIM2	Q8vim2 mus musculu	210	127	7.5	1249	2	Q90Z04	Q90z04 xenopus lae
138	133	7.9	349	1	LACH SCHAM	Q26474 schistocerc	211	127	7.5	1555	2	Q7P8H8	Q7p8h8 anopheles g
139	133	7.9	344	2	Q7ZXX1	Q7zxx1 xenopus lae	212	127	7.5	2053	2	Q8KXU7	Q8kxu7 homo sapien
140	133	7.9	463	2	BAC28450	Bac28450 m adult p	213	127	7.5	2092	2	Q76MU9	Q76mu9 homo sapien
141	133	7.9	463	2	BAC34294	Bac34294 m adult p	214	127	7.5	2092	2	BAAB6446	Baa66446 homo sapi
142	133	7.9	697	2	Q8NC72	Q8nc72 homo sapien	215	127	7.5	2113	2	Q8TDB4	Q8tdb4 homo sapien
143	133	7.9	1059	2	Q6UXL7	Q6uxl7 homo sapien	216	127	7.5	2133	2	Q7PQG9	Q7pqg9 anopheles g
144	133	7.9	1059	2	AAQ88662	AAq88662 homo sapi	217	126.5	7.5	442	2	Q6NM88	Q6nm88 brachydanio
145	133	7.9	1106	1	PGDR HUMAN	P09619 homo sapien	218	126.5	7.5	442	2	AAH67661	AAh67661 brachydan
146	133	7.9	1119	1	Q6UXM1	Q6uxm1 homo sapien	219	126.5	7.5	812	2	Q8N612	Q8n612 homo sapien
147	133	7.9	1119	1	AAQ88655	AAq88655 homo sapi	220	126.5	7.5	924	1	ICAS HUMAN	Q9unf0 homo sapien
148	132.5	7.8	298	2	Q9J159	Q9j159 m vascular	221	126.5	7.5	924	2	Q8TAM9	Q8tam9 homo sapien
149	132.5	7.8	298	2	AAH28778	AAh28778 mus muscu	222	126.5	7.5	1056	2	Q90Z03	Q90z03 xenopus lae
150	132.5	7.8	765	2	Q9TWA4	Q9twa4 aplysia cal	223	126	7.5	318	2	Q91664	Q91664 xenopus lae
151	132.5	7.8	765	2	Q9BKQ1	Q9bkq1 aplysia cal	224	126	7.5	413	2	Q7QBV2	Q7qbv2 anopheles g
152	132.5	7.8	812	2	Q9TWAS	Q9twas aplysia cal	225	126	7.5	539	2	BAC28314	Bac28314 m adult m
153	132.5	7.8	812	2	Q9BKQ0	Q9bkq0 aplysia cal	226	126	7.5	885	2	Q8HYV1	Q8hyv1 sus scrofa
154	132.5	7.8	932	2	Q9TWA6	Q9twa6 aplysia cal	227	126	7.5	886	2	Q8HYV2	Q8hyv2 sus scrofa
155	132.5	7.8	932	2	Q9BKP9	Q9bkp9 aplysia cal	228	126	7.5	948	2	Q9VME2	Q9vme2 drosophila
156	132.5	7.8	1369	1	NFAS CHICK	Q42414 gallus gall	229	126	7.5	948	2	AAFS2377	AAFS2377 drosophila
157	132	7.8	300	2	Q7SYQ7	Q7syq7 xenopus lae	230	126	7.5	1235	2	Q7Q0S7	Q7q0s7 anopheles g
158	132	7.8	1746	2	Q8WY19	Q8wy19 homo sapien	231	126	7.5	1431	2	Q8U060	Q8u060 mus musculu
159	132	7.8	2012	1	DSCA HUMAN	Q60469 homo sapien	232	125.5	7.4	303	2	Q7Q154	Q7q154 anopheles g
160	131.5	7.8	461	2	Q13854	Q13854 homo sapien	233	125.5	7.4	412	2	Q9R1E1	Q9r1e1 rattus norv
161	131.5	7.8	1117	2	Q6PIC6	Q6pic6 mus musculu	234	125.5	7.4	707	2	Q7PMU1	Q7pmu1 anopheles g
162	131.5	7.8	1117	2	AAH65142	AAh65142 mus muscu	235	125.5	7.4	1443	2	Q8WMB2	Q8wmb2 drosophila
163	131.5	7.8	2673	2	Q96SC3	Q96sc3 homo sapien	236	125.5	7.4	1496	2	Q92626	Q92626 homo sapien
164	131	7.8	289	2	Q9Y5B2	Q9y5b2 homo sapien	237	125.5	7.4	1765	2	Q9V830	Q9v830 drosophila
165	131	7.8	285	2	Q9D780	Q9d780 mus musculu	238	125.5	7.4	1770	2	Q9V829	Q9v829 drosophila
166	131	7.8	714	2	Q6ZPE6	Q6zpe6 mus musculu	239	125	7.4	313	2	Q5Y596	Q5y596 gallus gall
167	131	7.8	714	2	BAC98291	Bac98291 mus muscu	240	125	7.4	315	2	Q9DGI5	Q9dgi5 gallus gall
168	131	7.8	4391	1	PGEM HUMAN	P08160 homo sapien	241	125	7.4	1006	2	Q6IDB9	Q6idb9 drosophila
169	130.5	7.7	272	2	Q70J56	Q70j56 mus musculu	242	125	7.4	1006	2	AAE72780	AAe72780 drosophila
170	130	7.7	253	2	Q9DBH2	Q9dbh2 m mus muscu	243	124.5	7.4	259	2	Q7Z2Q1	Q7z2q1 homo sapien
171	130	7.7	285	1	Q8VE93	Q8ve93 mus musculu	244	124.5	7.4	344	2	Q93242	Q93242 gallus gall
172	130	7.7	515	1	PVRI PITG	Q9g176 sus scrofa	245	124.5	7.4	353	1	CEPU CHICK	Q90732 gallus gall
173	130	7.7	582	2	Q8R4B5	Q8r4b5 mus musculu	246	124.5	7.4	387	2	Q86XK7	Q86xk7 homo sapien
174	130	7.7	915	2	Q8R4B3	Q8r4b3 mus musculu	247	124.5	7.4	412	2	Q6WZS4	Q6wzs4 homo sapien
175	130	7.7	955	1	MDG1 HUMAN	Q8nfp4 homo sapien	248	124.5	7.4	412	2	CAE45954	Caee5954 homo sapi
176	129.5	7.7	1040	1	AXOI_RAT	P22063 rattus norv	249	124.5	7.4	877	2	Q9GSH3	Q9gsh3 halocynthia
177	129.5	7.7	1479	2	Q7KQTS	Q7kqts drosophila	250	124.5	7.4	1073	2	Q9W1T8	Q9wit8 drosophila

251	124.5	7.4	1173	2	06NR54	06nr54 drosophila	324	121.5	7.2	1299	2	AA89825	AA89825 rattus no
252	124.5	7.4	1173	2	AAQ23543	AAQ23543 homo sapien	325	121.5	7.2	1842	2	081ZY3	081zy3 homo sapien
253	124	7.3	311	2	06DN7	06dn7 xenopus lae	326	121	7.2	366	2	06NVZ3	06nvz3 homo sapi
254	124	7.3	394	2	06DC16	06dc16 pan troglod	327	121	7.2	366	2	AAH67808	AAH67808 homo sapi
255	124	7.3	597	1	SILV_PANTR	095110 pan troglod	328	121	7.2	410	2	07YZA7	07yza7 bombyx mori
256	124	7.3	623	2	08BY18	08by18 mus musculu	329	121	7.2	467	2	091VT9	091v9 mus musculu
257	124	7.3	688	2	080ZE3	080ze3 mus musculu	330	121	7.2	528	2	P91670	P91670 drosophila
258	124	7.3	697	2	07PMJ7	07pmj7 anopheles g	331	121	7.2	532	2	06NMU3	06nmu3 drosophila
259	124	7.3	853	1	NCAL_BOVIN	P1836 bos taurus	332	121	7.2	532	2	09YUFO	09yuf0 drosophila
260	124	7.3	1240	1	NPAS_HUMAN	Q91856 homo sapien	333	121	7.2	532	2	AAH88551	AAH88551 drosophila
261	124	7.3	1240	1	NPAS_MOUSE	Q81003 mus musculu	334	121	7.2	858	2	018466	018466 hirtudo medi
262	124	7.3	1240	1	NPAS_RAT	P97685 rattus norv	335	121	7.2	1031	2	090Y2M	090y2m brachydanio
263	124	7.3	1251	2	06Z054	06z054 mus musculu	336	121	7.2	1086	2	07OH02	07oh02 anopheles g
264	124	7.3	1251	2	BAC98017	Bac98017 mus muscu	337	121	7.2	1155	2	0703X8	0703x8 anopheles g
265	124	7.3	1366	1	ROB3_MOUSE	Q92214 mus musculu	338	121	7.2	1304	1	NRCA_HUMAN	092823 homo sapien
266	124	7.3	1730	2	07YRQ7	Q7yrt7 sus scrofa	339	120.5	7.1	163	3	08K1H8	08k1h8 mus musculu
267	123.5	7.3	316	2	07TPB4	Q7tpb4 rattus norv	340	120.5	7.1	202	2	06N7A1	06n7a1 homo sapien
268	123.5	7.3	338	1	LAMP_CHICK	Q98919 gallus gall	341	120.5	7.1	202	2	AAH69185	AAH69185 homo sapi
269	123.5	7.3	350	2	002869	002869 gallus gall	342	120.5	7.1	265	2	07PUY3	07puu3 anopheles g
270	123.5	7.3	383	2	075M19	Q75m19 gallus gall	343	120.5	7.1	358	2	090490	090490 brachydanio
271	123.5	7.3	383	2	AA507434	AA507434 homo sapi	344	120.5	7.1	440	2	AAQ88700	AAQ88700 homo sapi
272	123.5	7.3	412	2	063611	Q63611 rattus norv	345	120.5	7.1	442	1	SILV_HUMAN	043659 homo sapien
273	123.5	7.3	454	2	091W54	Q91w54 mus musculu	346	120.5	7.1	442	1	09BY67	09by67 homo sapien
274	123.5	7.3	521	1	CEAL_MOUSE	P31809 mus musculu	347	120.5	7.1	442	2	CAG33438	Cag33438 homo sapi
275	123.5	7.3	521	1	0925F3	Q925f3 mus musculu	348	120.5	7.1	482	2	BAC26124	Bac26124 mus muscu
276	123.5	7.3	605	2	0921P2	Q921p2 mus musculu	349	120.5	7.1	529	2	091V87	091v87 mus musculu
277	123.5	7.3	815	2	0805B9	Q805b9 brachydanio	350	120.5	7.1	529	2	AAH58745	AAH58745 mus muscu
278	123.5	7.3	838	2	08BQ96	Q8bq96 mus musculu	351	120.5	7.1	538	2	Q28939	Q28939 sus scrofa
279	123.5	7.3	838	2	08C4B2	Q8c4b2 mus musculu	352	120.5	7.1	549	2	09JUB9	09jub9 mus musculu
280	123.5	7.3	1091	1	NCAL_CHICK	P13590 gallus gall	353	120.5	7.1	1940	2	06PDN3	06pdn3 mus musculu
281	123.5	7.3	1151	1	090VNS	Q90vns rattus ap.	354	120.5	7.1	1940	2	AAH58610	AAH58610 mus muscu
282	123.5	7.3	1256	1	NRCA_MOUSE	Q81004 mus musculu	355	120	7.1	304	2	09BPN5	09bpn5 caenorhabdi
283	123	7.3	265	2	09NGZ0	Q9ngz0 spodoptera	356	120	7.1	312	2	06UXG6	06uxg6 homo sapien
284	123	7.3	344	1	NTRI_HUMAN	Q9p121 homo sapien	357	120	7.1	312	2	AAQ88727	AAQ88727 homo sapi
285	123	7.3	344	1	AAQ88697	AAQ88697 homo sapi	358	120	7.1	410	2	06R3L9	06r3l9 bombyx mand
286	123	7.3	439	2	057349	057349 xenopus gall	359	120	7.1	410	2	AA500446	AA500446 bombyx ma
287	123	7.3	464	2	06GL25	Q6gl25 xenopus tro	360	120	7.1	641	2	086SD2	086sd2 clona intes
288	123	7.3	538	2	Q29123	Q29123 sus scrofa	361	120	7.1	1033	2	Q24327	Q24327 drosophila
289	123	7.3	1247	2	07Q0S6	Q7q0s6 anopheles g	362	120	7.1	1033	2	09V643	09v643 drosophila
290	122.5	7.3	400	2	08HY16	Q8hy16 cebus apelli	363	120	7.1	1036	1	AXOI_CHICK	P28655 gallus gall
291	122.5	7.3	761	1	NCAL_HUMAN	P13592 homo sapien	364	120	7.1	1093	3	096V7A	Q96j11 homo sapien
292	122.5	7.3	848	1	NCAL_HUMAN	Q8hv66 brachydanio	365	119.5	7.1	1094	2	09BYB8	Q9byb8 homo sapien
293	122.5	7.3	1032	2	08UVD6	Q8uvd6 brachydanio	366	119.5	7.1	298	1	JAM2_HUMAN	P57087 homo sapien
294	122.5	7.3	1073	2	094898	Q94898 homo sapien	367	119.5	7.1	298	1	06VNC1	06vnc1 homo sapien
295	122.5	7.3	1284	1	NRCA_CHICK	P93531 gallus gall	368	119.5	7.1	298	2	AAH2538	AAH2538 homo sapi
296	122.5	7.3	1419	2	Q985W3	Q985w3 brachydanio	369	119.5	7.1	307	2	BAC35705	Bac35705 m 2 days
297	122.5	7.3	18412	2	Q7Z261	Q7z261 brachydanio	370	119.5	7.1	373	2	Q7KXP5	Q7kxp5 homo sapien
298	122	7.2	240	2	06MG96	Q6mg96 rattus norv	371	119.5	7.1	463	1	SILV_HUMAN	09y316 homo sapien
299	122	7.2	240	2	CAE83950	CAE83950 rattus no	372	119.5	7.1	464	2	Q16170	Q16170 homo sapien
300	122	7.2	410	2	06R3M2	Q6r3m2 bombyx mori	373	119.5	7.1	468	2	096CA7	Q96ca7 homo sapien
301	122	7.2	410	2	AA500443	AA500443 bombyx mo	374	119.5	7.1	483	2	09UFI4	Q9ufi4 homo sapien
302	122	7.2	433	2	06DJ83	Q6dj83 xenopus tro	375	119.5	7.1	526	1	CEAL_HUMAN	P13668 homo sapien
303	122	7.2	1166	2	09QVNA	Q9qvna rattus ap.	376	119.5	7.1	529	2	Q7TOM3	Q7tqm3 rattus norv
304	121.5	7.2	320	2	07QOP8	Q7qop8 anopheles g	377	119.5	7.1	549	2	Q9D006	Q9d006 mus musculu
305	121.5	7.2	344	1	CEA6_HUMAN	P40159 homo sapien	378	119.5	7.1	725	1	NCAL_MOUSE	P13554 mus musculu
306	121.5	7.2	344	2	AAH8776	AAH8776 homo sapi	379	119.5	7.1	725	1	073634	Q73634 xenopus lae
307	121.5	7.2	349	2	Q9NOS3	Q9ngs3 homo sapien	380	119.5	7.1	734	2	09NQT2	Q9ngt2 homo sapien
308	121.5	7.2	595	2	Q6ZRS5	Q6zrs5 homo sapien	381	119.5	7.1	1115	1	NCAL_MOUSE	P13555 mus musculu
309	121.5	7.2	595	2	BAC87234	Bac87234 homo sapi	382	119.5	7.1	1643	2	Q7QGT8	Q7qgt8 anopheles g
310	121.5	7.2	1154	2	09QVNA3	Q9qvna3 rattus ap.	383	119.5	7.1	1950	2	080YN8	Q80yn8 mus musculu
311	121.5	7.2	1194	2	06PM15	Q6pm15 rattus norv	384	119	7.0	334	2	002870	Q02870 gallus gall
312	121.5	7.2	1194	2	AA898824	AA898824 rattus no	385	119	7.0	337	2	P97268	P97268 cavia porce
313	121.5	7.2	1197	2	06PM38	Q6pm38 rattus norv	386	119	7.0	410	2	Q6R3M0	Q6r3m0 bombyx mori
314	121.5	7.2	1197	2	AA898821	AA898821 rattus no	387	119	7.0	410	2	AA500444	AA500444 bombyx mo
315	121.5	7.2	1198	2	06PM17	Q6pm17 rattus norv	388	119	7.0	410	2	AA500445	AA500445 bombyx mo
316	121.5	7.2	1198	2	AA898822	AA898822 rattus no	389	119	7.0	467	2	08C6F2	Q8c6f2 mus musculu
317	121.5	7.2	1206	2	06PM16	Q6pm16 rattus norv	390	119	7.0	727	2	06RKB2	Q6rkb2 rattus norv
318	121.5	7.2	1206	2	AA898823	AA898823 rattus no	391	119	7.0	727	2	AA818426	AA818426 rattus no
319	121.5	7.2	1209	2	06PM39	Q6pm39 rattus norv	392	119	7.0	779	2	097136	Q97136 manduca bex
320	121.5	7.2	1214	1	AA898820	AA898820 rattus no	393	119	7.0	837	2	097137	Q97137 manduca bex
321	121.5	7.2	1224	2	NRCA_RAT	P97686 rattus norv	394	119	7.0	837	2	Q6RKB3	Q6rkb3 rattus norv
322	121.5	7.2	1224	2	000573	000573 homo sapien	395	119	7.0	837	2	AA818425	AA818425 rattus no
323	121.5	7.2	1299	2	06PM14	Q6pm14 rattus norv	396	119	7.0	895	2	BAC34837	Bac34837 m 12 days

397	119	7.0	1091	2	P70193	P70193 mus musculus	470	117	6.9	448	2	O9JHL7	O9Jhl7 rattus norv
398	119	7.0	1994	2	O6ZPE2	O6ZPE2 mus musculus	471	117	6.9	459	2	O9JHL6	O9Jhl6 rattus norv
399	119	7.0	1994	2	BAC98189	BAC98189 mus muscu	472	117	6.9	595	1	SILL_HUMAN	O96q01 homo sapien
400	119	7.0	2176	2	O6V4S5	O6V4S5 mus musculus	473	117	6.9	739	1	VCA1_RAT	P29534 rattus norv
401	119	7.0	2176	2	AAQ57661	AAQ57661 mus muscu	474	117	6.9	858	1	NCA1_RAT	P13596 rattus norv
402	119	7.0	4463	2	O8MLD8	O8MLD8 drosophila	475	117	6.9	1062	2	O8BRG3	O8BRg3 mus musculus
403	119	7.0	9270	2	O8MLD9	O8MLD9 drosophila	476	117	6.9	1062	2	AAQ10071	AAQ10071 mus muscu
404	119	7.0	26926	2	O10466	O10466 homo sapien	477	117	6.9	1445	2	O63155	O63155 rattus norv
405	119	7.0	26926	2	O8WZB3	O8WZB3 homo sapien	478	117	6.9	1447	1	DCC_HUMAN	P43146 homo sapien
406	118.5	7.0	152	2	O8BSO8	O8BSO8 mus musculus	479	117	6.9	2164	2	O91AR9	O91ar9 gallus gall
407	118.5	7.0	282	2	O6UXZ0	O6UXZ0 homo sapien	480	116.5	6.9	285	2	O7PNT4	O7Pnt4 anopheles g
408	118.5	7.0	262	2	AAQ88520	AAQ88520 homo sapi	481	116.5	6.9	338	1	LAMP_RAT	O62813 rattus norv
409	118.5	7.0	282	2	O7TPU2	O7TPU2 mus musculus	482	116.5	6.9	341	2	O8BLK3	O8BLk3 mus musculus
410	118.5	7.0	282	2	O8VIM1	O8VIM1 mus musculus	483	116.5	6.9	361	2	O6VUH9	O6vuh9 rattus norv
411	118.5	7.0	333	1	AMAL_DROME	P15364 drosophila	484	116.5	6.9	361	2	AAQ91613	AAQ91613 rattus no
412	118.5	7.0	341	2	O7KSX2	O7KSX2 drosophila	485	116.5	6.9	445	2	O8K3T6	O8K3t6 mus musculus
413	118.5	7.0	341	2	AAH13372	AAH13372 drosophil	486	116.5	6.9	554	2	O9W4R3	O9W4r3 drosophila
414	118.5	7.0	413	2	O7OBU1	O7OBU1 anopheles g	487	116.5	6.9	806	1	CEK2_CHICK	P18460 gallus gall
415	118.5	7.0	439	2	O6GTV4	O6GTV4 homo sapien	488	116.5	6.9	899	2	O7PQM9	O7Pqm9 anopheles g
416	118.5	7.0	458	2	O63093	O63093 rattus norv	489	116.5	6.9	972	2	O26614	O26614 strongyloce
417	118.5	7.0	467	1	SIL7_HUMAN	O9Y286 homo sapien	490	116.5	6.9	1040	1	AXO1_HUMAN	O02246 homo sapien
418	118.5	7.0	510	2	O9ENV8	O9ENV8 homo sapien	491	116.5	6.9	1051	1	PXY7_CHICK	O91048 gallus gall
419	118.5	7.0	510	2	AAH10423	AAH10423 homo sapi	492	116.5	6.9	1598	2	O9P2I4	O9P2i4 homo sapien
420	118.5	7.0	519	1	BCTO_RAT	P16573 rattus norv	493	116	6.9	237	2	O6DOX5	O6dx5 oryctolagus
421	118.5	7.0	519	2	AAH61740	AAH61740 rattus no	494	116	6.9	344	1	NTRI_RAT	O62718 rattus norv
422	118.5	7.0	542	2	BAC27034	BAC27034 m adult m	495	116	6.9	1027	2	O9OW79	O9OW79 gallus gall
423	118.5	7.0	947	1	MUSK_CHICK	O8AXY6 gallus gall	496	116	6.9	1103	2	O6ONF3	O6onf3 canis fami
424	118.5	7.0	1011	2	O24273	O24273 drosophila	497	116	6.9	1103	2	AA548371	AA548371 canis fam
425	118.5	7.0	1476	2	O7Q029	O7Q029 anopheles g	498	116	6.9	1447	1	DCC_MOUSE	P70211 mus musculus
426	118.5	7.0	1561	2	O924D2	O924D2 mus musculus	499	116	6.9	1709	1	SN_HUMAN	O9B222 homo sapien
427	118.5	7.0	1694	1	SN_MOUSE	O62230 mus musculus	500	116	6.9	6658	2	O76281	O76281 drosophila
428	118	7.0	344	1	NTRI_MOUSE	O99010 mus musculus	501	116	6.9	8647	2	O7KOP5	O7KOP5 drosophila
429	118	7.0	344	2	O8BG33	O8BG33 m mus muscu	502	116	6.9	8647	2	AA564601	AA564601 drosophi
430	118	7.0	359	2	O7ZX17	O7ZX17 xenopus lae	503	116	6.9	8648	2	O7KOP6	O7KOP6 drosophi
431	118	7.0	391	2	O7Q0G1	O7Q0G1 anopheles g	504	116	6.9	8648	2	AA564600	AA564600 drosophi
432	118	7.0	413	2	O9VAR6	O9VAR6 drosophila	505	116	6.9	8930	2	O7KOP7	O7KOP7 drosophila
433	118	7.0	450	2	O9VAR25	O9VAR25 drosophila	506	116	6.9	8930	2	AA564599	AA564599 drosophi
434	118	7.0	501	2	O6Q147	O6Q147 bos taurus	507	116	6.9	8943	2	O9V4F7	O9V4f7 drosophila
435	118	7.0	501	2	AA573243	AA573243 bos tauri	508	115.5	6.8	295	2	O9Z2H8	O9Z2h8 mus musculus
436	118	7.0	540	2	O8NOZ9	O8NOZ9 homo sapien	509	115.5	6.8	295	2	O9OYL6	O9OYL6 mus musculus
437	118	7.0	547	1	ICA3_HUMAN	P32942 homo sapien	510	115.5	6.8	309	1	CD86_MOUSE	P42082 mus musculus
438	118	7.0	547	2	O6PD68	O6PD68 homo sapien	511	115.5	6.8	309	2	AA025880	AA025880 mus muscu
439	118	7.0	547	2	AAH58903	AAH58903 homo sapi	512	115.5	6.8	309	2	AA025881	AA025881 mus muscu
440	118	7.0	626	2	O6DCH3	O6dch3 xenopus lae	513	115.5	6.8	309	2	AA025882	AA025882 mus muscu
441	118	7.0	837	1	NCM2_MOUSE	O35136 mus musculus	514	115.5	6.8	309	2	AA025883	AA025883 mus muscu
442	118	7.0	1238	1	VGR1_HUMAN	P17948 h vascular	515	115.5	6.8	309	2	BAC37666	BAC37666 mus muscu
443	118	7.0	1238	2	O95YMI	O95YMI procambiarus	516	115.5	6.8	314	2	O61238	O61238 mus musculus
444	118	7.0	17352	2	O95YMI2	O95YMI2 procambiarus	517	115.5	6.8	356	2	O64381	O64381 mus musculus
445	117.5	7.0	309	2	O91YV7	O91YV7 mus musculus	518	115.5	6.8	390	2	O6P500	O6P500 rattus norv
446	117.5	7.0	316	2	O8VE98	O8VE98 mus musculus	519	115.5	6.8	390	2	AAH63181	AAH63181 rattus no
447	117.5	7.0	316	2	AAH56608	AAH56608 mus muscu	520	115.5	6.8	445	2	O8R4L1	O8R4L1 mus musculus
448	117.5	7.0	338	1	LAMP_HUMAN	O13449 homo sapien	521	115.5	6.8	520	2	O925P2	O925P2 mus musculus
449	117.5	7.0	338	2	O81V49	O81V49 homo sapien	522	115.5	6.8	725	2	O73633	O73633 xenopus lae
450	117.5	7.0	340	2	O9W3N2	O9W3N2 drosophila	523	115.5	6.8	734	2	O9NP65	O9NP65 homo sapien
451	117.5	7.0	342	2	O13774	O13774 homo sapien	524	115.5	6.8	734	2	O9NPB7	O9NPB7 homo sapien
452	117.5	7.0	437	2	AAH35359	AAH35359 homo sapi	525	115.5	6.8	734	2	O9NPQ9	O9NPQ9 homo sapien
453	117.5	7.0	509	2	O920C2	O920C2 mus musculus	526	115.5	6.8	734	2	O9NQS9	O9NQS9 homo sapien
454	117.5	7.0	775	2	O6PFS0	O6PFS0 xenopus lae	527	115.5	6.8	734	2	O9NQTO	O9NQTO homo sapien
455	117.5	7.0	775	2	AAH57728	AAH57728 xenopus l	528	115.5	6.8	734	2	O9NQTI	O9NQTI homo sapien
456	117.5	7.0	800	2	O918X3	O918X3 brachydantio	529	115.5	6.8	734	2	O96RFS	O96Rf5 homo sapien
457	117.5	7.0	858	2	O86X47	O86X47 homo sapien	530	115.5	6.8	734	2	O96RFS	O96Rf6 homo sapien
458	117.5	7.0	1028	2	P97528	P97528 rattus norv	531	115.5	6.8	738	1	PECL_HUMAN	P16284 homo sapien
459	117.5	7.0	1056	2	O7ZW34	O7ZW34 brachydantio	532	115.5	6.8	738	1	O8TBH1	O8TBH1 homo sapien
460	117.5	7.0	1092	1	NCA2_XENTLA	P36335 xenopus lae	533	115.5	6.8	1252	2	O96DN3	O96dn3 homo sapien
461	117.5	7.0	1302	1	NRG_DROME	P20241 drosophila	534	115.5	6.8	1255	2	O723Z9	O723Z9 homo sapien
462	117.5	7.0	1389	2	O90Z69	O90Z69 brachydantio	535	115.5	6.8	1255	2	O7YQL8	O7Yql8 pan troglod
463	117.5	7.0	2008	2	O9VEJ5	O9VEJ5 drosophila	536	115.5	6.8	1257	1	CAML_HUMAN	P32004 homo sapien
464	117.5	7.0	2046	2	O7KSG9	O7KSG9 drosophila	537	115.5	6.8	1493	1	NEO1_MOUSE	P97798 mus musculus
465	117.5	7.0	2046	2	AA565164	AA565164 drosophi	538	115.5	6.8	4001	2	O9N2F7	O9N2F7 drosophila
466	117.5	7.0	8625	2	O86GD6	O86GD6 procambiarus	539	115.5	6.8	4796	2	O9N055	O9N055 drosophila
467	117	6.9	351	2	O6WEB2	O6WEB2 branchiosto	540	115.5	6.8	4796	2	O9NLE8	O9NLE8 drosophila
468	117	6.9	351	2	AA057589	AA057589 branchios	541	115.5	6.8	16215	2	O9NFS3	O9Nf3 drosophila
469	117	6.9	401	2	O7PSS8	O7PSS8 anopheles g	542	115.5	6.8	17903	2	O7RTL4	O7RTL4 drosophila

543	115.5	6.8	18074	2	O917U4	O917U4	drosoophila	616	113.5	6.7	530	2	O80XJ5	O80XJ5	mus musculus
544	115	6.8	217	2	O6KGN0	O6KGN0	bacterioph	617	113.5	6.7	754	2	O8BZ76	O8BZ76	m mus muscu
545	115	6.8	237	2	O8CG82	O8CG82	mus musculi	618	113.5	6.7	771	2	O7Q3H8	O7Q3H8	anopheles g
546	115	6.8	294	2	O6KGN1	O6KGN1	bacterioph	619	113.5	6.7	875	2	O91ZV7	O91ZV7	mus musculi
547	115	6.8	306	2	O9QYL4	O9QYL4	mus musculi	620	113.5	6.7	939	2	O9VB35	O9VB35	drosoophila
548	115	6.8	316	2	O8WPM3	O8WPM3	drosoophila	621	113.5	6.7	939	2	O967X6	O967X6	drosoophila
549	115	6.8	399	2	O8N772	O8N772	drosoophila	622	113.5	6.7	1248	2	O9XT41	O9XT41	cercopthec
550	115	6.8	424	2	O8CEW0	O8CEW0	mus musculi	623	113.5	6.7	1255	2	O7YQJ7	O7YQJ7	pongo pygma
551	115	6.8	602	2	O86Y09	O86Y09	mus musculi	624	113.5	6.7	1386	2	ROB3_HUMAN	ROB3_HUMAN	homo sapien
552	115	6.8	650	2	O8NAB4	O8NAB4	homo sapien	625	113.5	6.7	1614	2	O8UDV7	O8UDV7	anopheles lae
553	115	6.8	731	2	O8SP16	O8SP16	macroopus eu	626	113.5	6.7	1675	2	O98SW4	O98SW4	brachydanio
554	115	6.8	837	2	O7Z7F2	O7Z7F2	homo sapien	627	113	6.7	336	1	C226_HUMAN	C226_HUMAN	homo sapien
555	115	6.8	1125	2	O7QEC1	O7QEC1	anopheles g	628	113	6.7	340	2	O7Q8Q7	O7Q8Q7	anopheles g
556	115	6.8	1209	1	P70232	P70232	mus musculi	629	113	6.7	538	2	O9NM07	O9NM07	homo sapien
557	115	6.8	1302	1	VER2_BRABE	VER2_BRABE	brachydanio	630	113	6.7	1109	2	O6P5H3	O6P5H3	mus musculi
558	115	6.8	1723	2	O8CHB2	O8CHB2	mus musculi	631	113	6.7	1109	2	AAH62892	AAH62892	mus muscu
559	115	6.8	2403	2	O8MLD5	O8MLD5	drosoophila	632	113	6.7	1277	1	CAML_FURRU	CAML_FURRU	fugu rubrip
560	115	6.8	7210	2	O9V7G8	O9V7G8	drosoophila	633	113	6.7	3100	2	O7KYN5	O7KYN5	homo sapien
561	114.5	6.8	163	2	O9NVJ5	O9NVJ5	homo sapien	634	113	6.7	4650	2	O15598	O15598	homo sapien
562	114.5	6.8	345	2	O6GM08	O6GM08	anopheles lae	635	112.5	6.7	226	2	O7PYG1	O7PYG1	anopheles g
563	114.5	6.8	363	2	O6NV41	O6NV41	brachydanio	636	112.5	6.7	244	2	O957B9	O957B9	drosoophila
564	114.5	6.8	363	2	AAH68325	AAH68325	brachydan	637	112.5	6.7	338	2	O7Z3W6	O7Z3W6	homo sapien
565	114.5	6.8	412	2	O8HY14	O8HY14	oryctolagus	638	112.5	6.7	345	1	OPCM_HUMAN	OPCM_HUMAN	homo sapien
566	114.5	6.8	458	2	O61351	O61351	mus musculi	639	112.5	6.7	362	2	O9JHQ1	O9JHQ1	rattus norv
567	114.5	6.8	479	2	CAG33099	CAG33099	homo sapi	640	112.5	6.7	363	2	O46147	O46147	onchocerca
568	114.5	6.8	489	2	O7PGL7	O7PGL7	anopheles g	641	112.5	6.7	401	2	O08835	O08835	cercopthec
569	114.5	6.8	497	2	O9BXN7	O9BXN7	homo sapien	642	112.5	6.7	440	2	O6ZMD4	O6ZMD4	homo sapien
570	114.5	6.8	499	1	SLR_HUMAN	SLR_HUMAN	homo sapien	643	112.5	6.7	440	2	BAD18794	BAD18794	homo sapi
571	114.5	6.8	504	2	O8N441	O8N441	homo sapien	644	112.5	6.7	517	1	PVRL_HUMAN	PVRL_HUMAN	homo sapien
572	114.5	6.8	504	2	O9HAD7	O9HAD7	homo sapien	645	112.5	6.7	743	2	O6R6B2	O6R6B2	vibriophag
573	114.5	6.8	504	2	AAO88670	AAO88670	homo sapi	646	112.5	6.7	743	2	AAH92067	AAH92067	vibrioph
574	114.5	6.8	521	2	O61352	O61352	mus musculi	647	112.5	6.7	782	2	O61563	O61563	mus musculi
575	114.5	6.8	538	1	PVR2_HUMAN	PVR2_HUMAN	homo sapien	648	112.5	6.7	1070	2	O61Q51	O61Q51	homo sapien
576	114.5	6.8	551	2	O8MSN7	O8MSN7	drosoophila	649	112.5	6.7	1259	1	CAML_RAT	CAML_RAT	rattus norv
577	114.5	6.8	956	2	O9W4T9	O9W4T9	drosoophila	650	112.5	6.7	1259	2	O9QY38	O9QY38	mus musculi
578	114.5	6.8	959	2	O9N9Y9	O9N9Y9	drosoophila	651	112.5	6.7	1259	2	AAH56988	AAH56988	mus muscu
579	114.5	6.8	975	2	O97174	O97174	drosoophila	652	112.5	6.7	1342	2	O9VP27	O9VP27	drosoophila
580	114.5	6.8	1088	1	NCA1_XENLA	NCA1_XENLA	anopheles lae	653	112.5	6.7	1342	2	O9GPP6	O9GPP6	drosoophila
581	114.5	6.8	1415	2	O94155	O94155	caenorhabd	654	112.5	6.7	2029	1	IAR_DRONE	IAR_DRONE	drosoophila
582	114.5	6.8	1415	2	AAH37634	AAH37634	caenorhab	655	112.5	6.7	2029	2	O9VIS8	O9VIS8	drosoophila
583	114.5	6.8	5604	2	O8W253	O8W253	homo sapien	656	112.5	6.7	2224	2	O9UIM1	O9UIM1	drosoophila
584	114	6.8	235	2	O75296	O75296	homo sapien	657	112	6.6	316	2	O8WP94	O8WP94	drosoophila
585	114	6.8	337	2	O6DPY2	O6DPY2	mus musculi	658	112	6.6	355	2	O7Z3B1	O7Z3B1	homo sapien
586	114	6.8	403	2	O8HY15	O8HY15	lemur catta	659	112	6.6	456	2	O8R5M8	O8R5M8	mus musculi
587	114	6.8	438	2	O9JLB7	O9JLB7	mus musculi	660	112	6.6	590	2	O6P4T5	O6P4T5	mus musculi
588	114	6.8	483	2	O9DBP8	O9DBP8	mus musculi	661	112	6.6	590	2	AAH63257	AAH63257	mus muscu
589	114	6.8	508	2	O8CED8	O8CED8	mus musculi	662	112	6.6	913	2	O8T3B5	O8T3B5	caenorhabd
590	114	6.8	508	2	O8R007	O8R007	mus musculi	663	112	6.6	928	2	O19128	O19128	caenorhabd
591	114	6.8	510	2	O9JLB8	O9JLB8	mus musculi	664	112	6.6	946	2	O07153	O07153	torpedo cal
592	114	6.8	544	1	ICAJ3_BOVIN	ICAJ3_BOVIN	bos taurus	665	112	6.6	955	2	O8WQ86	O8WQ86	caenorhabd
593	114	6.8	545	2	O9VCT4	O9VCT4	drosoophila	666	112	6.6	1212	2	O95TG0	O95TG0	drosoophila
594	114	6.8	672	2	O8IP70	O8IP70	drosoophila	667	112	6.6	1269	2	O01632	O01632	caenorhabd
595	114	6.8	672	2	AAQ23561	AAQ23561	drosoophila	668	112	6.6	1273	2	O44928	O44928	caenorhabd
596	114	6.8	795	2	O90YMO	O90YMO	brachydanio	669	112	6.6	1386	2	O8T172	O8T172	methanosarc
597	114	6.8	1028	2	O8CEX1	O8CEX1	mus musculi	670	111.5	6.6	267	2	O8NC05	O8NC05	homo sapien
598	114	6.8	1028	2	O9JMB8	O9JMB8	mus musculi	671	111.5	6.6	350	2	O95XK3	O95XK3	homo sapien
599	114	6.8	1045	2	O86T37	O86T37	homo sapien	672	111.5	6.6	400	1	HPL4_MOUSE	HPL4_MOUSE	macaca fasc
600	114	6.8	1073	2	O9TXI8	O9TXI8	caenorhabd	673	111.5	6.6	508	2	O96L45	O96L45	homo sapien
601	114	6.8	1177	2	O6GDB1	O6GDB1	anopheles lae	674	111.5	6.6	421	2	AAQ88499	AAQ88499	homo sapi
602	114	6.8	1320	2	O86TC9	O86TC9	homo sapien	675	111.5	6.6	421	2	O7PV30	O7PV30	anopheles g
603	114	6.8	1320	2	O96KFS	O96KFS	homo sapien	676	111	6.6	1060	2	O9QZL3	O9QZL3	anopheles g
604	114	6.8	1735	2	O7Q916	O7Q916	anopheles g	677	111	6.6	283	2	O8XQ91	O8XQ91	mus musculi
605	113.5	6.7	232	2	O7PJ18	O7PJ18	anopheles g	678	111	6.6	352	2	O6U706	O6U706	homo sapien
606	113.5	6.7	284	2	O9NX42	O9NX42	homo sapien	679	111	6.6	352	2	AAQ88499	AAQ88499	homo sapi
607	113.5	6.7	296	2	O6PJ56	O6PJ56	homo sapien	680	111	6.6	421	2	O7PV30	O7PV30	anopheles g
608	113.5	6.7	296	2	AAH22317	AAH22317	homo sapi	681	111	6.6	421	2	O7OLK4	O7OLK4	anopheles g
609	113.5	6.7	327	2	O961Q7	O961Q7	homo sapien	682	111	6.6	474	2	O7PKB3	O7PKB3	anopheles g
610	113.5	6.7	327	2	AAQ89256	AAQ89256	homo sapi	683	111	6.6	527	2	O9ERP7	O9ERP7	cricetus
611	113.5	6.7	382	2	O7PSH7	O7PSH7	anopheles g	684	111	6.6	593	2	O7Z696	O7Z696	homo sapien
612	113.5	6.7	482	2	BAC29175	BAC29175	homo sapien	685	111	6.6	769	2	O8N115	O8N115	homo sapien
613	113.5	6.7	499	2	O7Z728	O7Z728	homo sapien	686	111	6.6	806	1	FGR3_HUMAN	FGR3_HUMAN	homo sapien
614	113.5	6.7	510	2	O96K15	O96K15	homo sapien	687	111	6.6	807	2	O6NYZ3	O6NYZ3	brachydanio
615	113.5	6.7	530	1	PVR2_MOUSE	PVR2_MOUSE	mus musculi	688	111	6.6	907	2	AAH6766	AAH6766	brachydan

689	11.1	6.6	960	2	Q7PV74	Q7PV74 anopheles g	762	109	6.5	562	2	AA11440	AA11440 brachydian
690	11.1	6.6	1036	2	Q81WV2	Q81WV2 homo sapien	763	109	6.5	640	2	Q8BSM2	Q8BSM2 mus musculus
691	11.1	6.6	1228	2	Q8MRA3	Q8MRA3 drosophila	764	109	6.5	646	1	MU18_HUMAN	P43121 homo sapien
692	11.1	6.6	1228	2	AAE58172	AAE58172 drosophila	765	109	6.5	646	2	Q6PHE3	Q6PHE3 homo sapien
693	11.1	6.6	1235	2	Q86BD5	Q86BD5 drosophila	766	109	6.5	646	2	AAH56418	AAH56418 homo sapi
694	11.1	6.6	1235	2	Q9V787	Q9V787 drosophila	767	109	6.5	1106	2	Q8WX93	Q8WX93 homo sapien
695	11.1	6.6	6632	1	UN89_CAEEL	001761 caenorhabdi	768	108.5	6.4	329	2	BAC28982	BAC28982 mus muscu
696	11.1	6.6	8081	2	Q72120	Q72120 caenorhabdi	769	108.5	6.4	345	1	OPCM_BOVIN	P1834 bos taurus
697	110.5	6.5	370	2	Q6MZ03	Q6MZ03 homo sapien	770	108.5	6.4	348	1	KIT0_RAT	Q92018 rattus norv
698	110.5	6.5	370	2	CAE45975	CAE45975 homo sapi	771	108.5	6.4	348	2	Q80224	Q80224 mus musculus
699	110.5	6.5	330	2	Q96AP7	Q96AP7 homo sapien	772	108.5	6.4	416	2	Q7M048	Q7M048 rattus norv
700	110.5	6.5	390	2	Q96T50	Q96T50 homo sapien	773	108.5	6.4	495	2	Q8HCY1	Q8HCY1 homo sapien
701	110.5	6.5	330	2	AAQ88748	AAQ88748 homo sapi	774	108.5	6.4	705	2	Q8CBD3	Q8CBD3 mus musculus
702	110.5	6.5	422	2	Q96PJ3	Q96PJ3 homo sapien	775	108.5	6.4	878	2	Q9GU22	Q9GU22 mytilus gal
703	110.5	6.5	513	2	Q00481	Q00481 homo sapien	776	108.5	6.4	1028	2	Q9U052	Q9U052 homo sapien
704	110.5	6.5	515	2	Q96BJ5	Q96BJ5 homo sapien	777	108.5	6.4	1114	2	Q9BMV1	Q9BMV1 homo sapien
705	110.5	6.5	515	2	Q96BJ5	Q96BJ5 homo sapien	778	108.5	6.4	1115	2	Q6UXJ5	Q6UXJ5 homo sapien
706	110.5	6.5	544	2	Q6UX18	Q6UX18 homo sapien	779	108.5	6.4	1115	2	AAQ88694	AAQ88694 homo sapi
707	110.5	6.5	544	2	AAQ88703	AAQ88703 homo sapi	780	108.5	6.4	1328	2	Q21043	Q21043 caenorhabdi
708	110.5	6.5	717	2	AAQ88495	AAQ88495 homo sapi	781	108.5	6.4	2000	2	Q97791	Q97791 oryctolagus
709	110.5	6.5	816	2	Q91285	Q91285 pleurodeles	782	108.5	6.4	2169	2	Q8AV58	Q8AV58 gallus gall
710	110.5	6.5	1070	1	PTK7_HUMAN	Q13308 homo sapien	783	108.5	6.4	4203	2	Q955G2	Q955G2 caenorhabdi
711	110.5	6.5	1189	2	Q9P2J2	Q9P2J2 homo sapien	784	108.5	6.4	4219	2	Q9ND87	Q9ND87 caenorhabdi
712	110.5	6.5	1889	2	Q7Q0X2	Q7Q0X2 anopheles g	785	108.5	6.4	4369	2	Q8MXD7	Q8MXD7 caenorhabdi
713	11.0	6.5	218	2	Q6ZMC6	Q6ZMC6 homo sapien	786	108.5	6.4	4447	2	Q8MXD8	Q8MXD8 caenorhabdi
714	11.0	6.5	218	2	BAD18803	BAD18803 homo sapi	787	108.5	6.4	4488	2	Q9TXK2	Q9TXK2 caenorhabdi
715	11.0	6.5	316	2	Q9BXR1	Q9BXR1 homo sapien	788	108.5	6.4	4736	2	Q7Y799	Q7Y799 mytilus gal
716	11.0	6.5	483	2	Q7SX76	Q7SX76 brachydanio	789	108	6.4	173	2	Q9JKD5	Q9JKD5 rattus norv
717	11.0	6.5	636	2	Q22040	Q22040 caenorhabdi	790	108	6.4	286	2	Q46535	Q46535 bos taurus
718	11.0	6.5	741	2	Q6RCF4	Q6RCF4 vibrifophage	791	108	6.4	325	2	Q95791	Q95791 homo sapien
719	11.0	6.5	741	2	AAE97631	AAE97631 vibrifoph	792	108	6.4	325	2	Q8HW98	Q8HW98 mus musculus
720	11.0	6.5	815	2	Q8AYP3	Q8AYP3 brachydanio	793	108	6.4	329	2	Q8H225	Q8H225 homo sapien
721	11.0	6.5	816	2	Q8NPF5	Q8NPF5 homo sapien	794	108	6.4	333	2	Q8NAQ3	Q8NAQ3 branchiosteo
722	11.0	6.5	837	1	NCM2_HUMAN	Q15394 homo sapien	795	108	6.4	354	2	Q8NAQ3	Q8NAQ3 homo sapien
723	11.0	6.5	917	1	ICAE_MOUSE	Q60625 mus musculus	796	108	6.4	376	2	Q90271	Q90271 brachydanio
724	11.0	6.5	1070	2	Q61Q54	Q61Q54 homo sapien	797	108	6.4	509	2	Q9EQY5	Q9EQY5 w lman-9 pr
725	11.0	6.5	1070	2	AAH04862	AAH04862 homo sapi	798	108	6.4	526	1	BUTY_BOVIN	Q9EY65 bos taurus
726	11.0	6.5	1070	2	AAH71557	AAH71557 homo sapi	799	108	6.4	614	2	Q6DDQ7	Q6DDQ7 xenopus lae
727	11.0	6.5	1097	1	PGDR_RAT	Q05010 rattus norv	800	108	6.4	868	1	MUSK_RAT	Q62318 rattus norv
728	11.0	6.5	1378	1	ROB2_HUMAN	Q9HCK4 homo sapien	801	109	6.4	1099	2	P97527	P97527 rattus norv
729	11.0	6.5	1391	2	Q8N3L4	Q8N3L4 homo sapien	802	108	6.4	1150	2	Q8BS24	Q8BS24 mus musculus
730	11.0	6.5	1880	2	Q18465	Q18465 hirtudo medi	803	108	6.4	2225	2	Q9N3X8	Q9N3X8 caenorhabdi
731	11.0	6.5	2389	2	Q6BEO6	Q6BEO6 caenorhabdi	804	107.5	6.4	270	2	BAC26003	BAC26003 mus muscu
732	109.5	6.5	333	2	Q9BDM2	Q9BDM2 cercopithe	805	107.5	6.4	288	2	BAC29632	BAC29632 mus muscu
733	109.5	6.5	333	1	C226_MOUSE	Q8K4F0 mus musculus	806	107.5	6.4	323	2	Q9BDB8	Q9BDB8 cercocobus
734	109.5	6.5	334	2	Q819N0	Q819N0 branchiosteo	807	107.5	6.4	350	2	Q99420	Q99420 homo sapien
735	109.5	6.5	345	1	OPCM_RAT	P32736 rattus norv	808	107.5	6.4	350	2	Q819N1	Q819N1 branchiosteo
736	109.5	6.5	349	1	CEAB_HUMAN	P31997 homo sapien	809	107.5	6.4	366	2	Q8N759	Q8N759 homo sapien
737	109.5	6.5	333	2	Q7QBC5	Q7QBC5 anopheles g	810	107.5	6.4	402	1	HP14_HUMAN	Q86UW8 homo sapien
738	109.5	6.5	430	2	Q7QGS8	Q7QGS8 anopheles g	811	107.5	6.4	428	2	Q96PJ6	Q96PJ6 homo sapien
739	109.5	6.5	435	2	Q8N3J6	Q8N3J6 anopheles g	812	107.5	6.4	429	2	Q96LA6	Q96LA6 homo sapien
740	109.5	6.5	477	2	Q6UXJ4	Q6UXJ4 homo sapien	813	107.5	6.4	605	2	Q6GNL9	Q6GNL9 xenopus lae
741	109.5	6.5	477	2	AAQ88696	AAQ88696 homo sapi	814	107.5	6.4	659	2	Q6ZNM1	Q6ZNM1 homo sapien
742	109.5	6.5	526	1	BUTY_HUMAN	Q13410 homo sapien	815	107.5	6.4	659	2	BAC85123	BAC85123 homo sapi
743	109.5	6.5	526	2	Q9H458	Q9H458 homo sapien	816	107.5	6.4	660	2	Q72681	Q72681 homo sapien
744	109.5	6.5	595	2	Q90720	Q90720 gallus gall	817	107.5	6.4	1026	2	Q62845	Q62845 rattus norv
745	109.5	6.5	1336	1	VGR1_RAT	P53767 rattus norv	818	107.5	6.4	1225	2	Q6GPE1	Q6GPE1 xenopus lae
746	109.5	6.5	1465	2	Q7TQG5	Q7TQG5 mus musculus	819	107.5	6.4	1235	2	Q95428	Q95428 homo sapien
747	109	6.5	263	2	Q7TPM5	Q7TPM5 mus musculus	820	107	6.3	199	2	Q8ND10	Q8ND10 homo sapien
748	109	6.5	283	2	Q7TPH5	Q7TPH5 mus musculus	821	107	6.3	332	2	Q6UXG3	Q6UXG3 homo sapien
749	109	6.5	283	2	Q7TSP5	Q7TSP5 mus musculus	822	107	6.3	332	2	AAQ88730	AAQ88730 homo sapi
750	109	6.5	283	2	AAQ24205	AAQ24205 mus muscu	823	107	6.3	437	2	Q8NPF6	Q8NPF6 homo sapien
751	109	6.5	292	2	Q6UY47	Q6UY47 homo sapien	824	107	6.3	442	2	Q6KAT6	Q6KAT6 mus musculus
752	109	6.5	292	2	AAQ88451	AAQ88451 homo sapi	825	107	6.3	442	2	BAD21371	BAD21371 mus muscu
753	109	6.5	316	2	Q8MP58	Q8MP58 drosophila	826	107	6.3	449	2	Q9UE16	Q9UE16 homo sapien
754	109	6.5	328	2	Q88775	Q88775 rattus norv	827	107	6.3	515	1	PVRI_MOUSE	Q9JKE6 mus musculus
755	109	6.5	336	2	AAH61846	AAH61846 rattus no	828	107	6.3	515	2	Q6P9M9	Q6P9M9 mus musculus
756	109	6.5	336	2	Q46551	Q46551 hyllobates s	829	107	6.3	515	2	AAH60694	AAH60694 mus muscu
757	109	6.5	345	2	Q7PVU1	Q7PVU1 anopheles g	830	107	6.3	606	2	Q9JSS8	Q9JSS8 rattus norv
758	109	6.5	437	2	Q81ZP8	Q81ZP8 homo sapien	831	107	6.3	622	2	Q9JKB2	Q9JKB2 mus musculus
759	109	6.5	547	1	CD19_MOUSE	P25918 mus musculus	832	107	6.3	648	2	Q9EPF2	Q9EPF2 rattus norv
760	109	6.5	547	1	BAC40973	BAC40973 mus muscu	833	107	6.3	773	1	PIGR_RABIT	P01332 oryctolagus
761	109	6.5	562	2	Q6VYR7	Q6VYR7 brachydanio	834	107	6.3	817	2	Q8UG38	Q8UG38 brachydanio

835	107	6.3	2558	2	06NR91	06nr91 drosophila
836	107	6.3	2558	2	AR88555	Ar88555 drosophila
837	107	6.3	19066	2	0801W8	0801w8 brachydanio
838	106.5	6.3	289	2	09QYL5	09qyl5 mus musculus
839	106.5	6.3	304	2	09CVA4	09cva4 mus musculus
840	106.5	6.3	354	1	HPL1 HORSE	028381 equus caball
841	106.5	6.3	437	2	086YV1	086yv1 homo sapien
842	106.5	6.3	546	2	080X70	080x70 mus musculus
843	106.5	6.3	548	2	09NR33	09nr33 mus musculus
844	106.5	6.3	719	2	09U4G1	09u4g1 drosophila
845	106.5	6.3	719	2	AAFS1028	Aaf51028 drosophila
846	106.5	6.3	793	2	070246	070246 mus musculus
847	106.5	6.3	813	2	08B0C3	08b0c3 mus musculus
848	106.5	6.3	1227	2	021038	021038 caenorhabdi
849	106.5	6.3	1232	2	090284	090284 carassius a
850	106	6.3	316	2	06UX12	06ux12 homo sapien
851	106	6.3	316	2	AAQ88709	Aa88709 homo sapi
852	106	6.3	317	2	08BER4	08ber4 cormox viru
853	106	6.3	381	2	08R4R1	08r4r1 mus musculus
854	106	6.3	407	2	09D234	09d234 mus musculus
855	106	6.3	582	2	080W2	080w2 mus musculus
856	106	6.3	907	2	09NEG0	09neg0 drosophila
857	106	6.3	919	2	07JPR6	07jpr6 caenorhabdi
858	106	6.3	919	2	07KXP0	07kxp0 caenorhabdi
859	106	6.3	947	2	044171	044171 caenorhabdi
860	106	6.3	947	2	026262	026262 caenorhabdi
861	106	6.3	1040	1	BS15 CAEBL	010655 caenorhabdi
862	106	6.3	1051	2	07JL68	07j168 caenorhabdi
863	106	6.3	1051	2	CAE47468	Ca47468 caenorhab
864	106	6.3	1096	2	08MO14	08mo14 caenorhabdi
865	106	6.3	1098	1	PGDR MOUSE	P05622 mus musculus
866	106	6.3	1109	2	08CR51	08ce51 mus musculus
867	106	6.3	1110	2	08CR73	08ce73 mus musculus
868	106	6.3	1409	2	0801M2	0801m2 brachydanio
869	106	6.3	1409	2	08J127	08j127 brachydanio
870	106	6.3	1428	2	08AY67	08ay67 brachydanio
871	106	6.3	1474	2	08T4W0	08t4w0 drosophila
872	106	6.3	1509	2	08IRP1	08irp1 drosophila
873	106	6.3	1509	2	09SP10	09sp10 drosophila
874	106	6.3	1914	1	KML5 HUMAN	015746 homo sapien
875	106	6.3	1914	2	07Z4U0	07z4j0 homo sapien
876	106	6.3	2222	2	07QEG7	07qeg7 anopheles g
877	105.5	6.2	318	2	08AY28	08ay28 variola vir
878	105.5	6.2	318	2	08BRT5	08brt5 variola vir
879	105.5	6.2	328	2	09Z109	09z109 mus musculus
880	105.5	6.2	394	2	06UXG0	06uxg0 homo sapien
881	105.5	6.2	394	2	AAQ88735	Aa88735 homo sapi
882	105.5	6.2	408	2	08BVP6	08bvp6 mus musculus
883	105.5	6.2	408	2	08K094	08k094 m hypotherci
884	105.5	6.2	408	2	091WP1	091wp1 mus musculus
885	105.5	6.2	485	1	FODX_RAT	09wcq2 rattus norv
886	105.5	6.2	525	2	07PZ58	07p288 anopheles g
887	105.5	6.2	527	2	06ZTR2	06ztr2 homo sapien
888	105.5	6.2	527	2	BAC86520	Bac86520 homo sapi
889	105.5	6.2	626	1	MAG_RAT	P07722 rattus norv
890	105.5	6.2	729	2	063827	063827 rattus sp.
891	105.5	6.2	731	2	08CFR8	08cfr8 mus musculus
892	105.5	6.2	733	2	060830	060830 mus musculus
893	105.5	6.2	733	2	080T10	080t10 mus musculus
894	105.5	6.2	789	2	07PME2	07pme2 anopheles g
895	105.5	6.2	789	2	08CIM9	08cim9 mus musculus
896	105.5	6.2	822	1	FGRI_HUMAN	P11362 homo sapien
897	105.5	6.2	822	1	FGRI_MOUSE	P16092 mus musculus
898	105.5	6.2	822	1	FGRI_RAT	Q04589 rattus norv
899	105.5	6.2	822	2	060818	060818 mus musculus
900	105.5	6.2	822	2	AA579322	Aa579322 homo sapi
901	105.5	6.2	869	1	MUSK_HUMAN	015146 homo sapien
902	105.5	6.2	987	2	07YZM6	07yzm6 caenorhabdi
903	105.5	6.2	988	2	CAC70094	Ca70094 caenorhab
904	105.5	6.2	1036	2	08SMW3	08smw3 drosophila
905	105.5	6.2	1102	2	0923W7	0923w7 mus musculus
906	105.5	6.2	1390	2	09VN14	09vn14 drosophila
907	105	6.2	145	2	09MZE4	09mze4 macaca mula
908	105	6.2	232	2	08BZ74	08bz74 mus musculus
909	105	6.2	408	2	09VTR3	09vtr3 drosophila
910	105	6.2	509	2	091YK7	091yk7 mus musculus
911	105	6.2	533	2	08NCB6	08ncb6 homo sapien
912	105	6.2	622	2	09R069	09r069 mus musculus
913	105	6.2	622	2	09ESS5	09ess5 mus musculus
914	105	6.2	646	2	095812	095812 homo sapien
915	105	6.2	650	2	099X86	099x86 mus musculus
916	105	6.2	662	2	08M229	08m229 drosophila
917	105	6.2	662	2	09VGD0	09vgd0 drosophila
918	105	6.2	724	2	003836	003836 xenopus lae
919	105	6.2	739	2	0865F2	0865f2 cycctolagus
920	105	6.2	800	2	09JHX9	09jhx9 rattus norv
921	105	6.2	810	2	09PS96	09ps96 xenopus lae
922	105	6.2	828	2	09DGK3	09dgk3 xenopus lae
923	105	6.2	988	2	0977Y2	0977y2 thermoplasm
924	105	6.2	1066	2	08MSR5	08msr5 drosophila
925	105	6.2	1215	2	07KTI7	07kti7 drosophila
926	105	6.2	1215	2	AA564657	Aa564657 drosophila
927	105	6.2	1461	2	08T9P6	08t9p6 drosophila
928	105	6.2	1503	2	07KTI8	07kti8 drosophila
929	105	6.2	1503	2	AA564655	Aa564655 drosophila
930	105	6.2	1509	2	09VLQ8	09vlq8 drosophila
931	105	6.2	3215	2	08IRV7	08irv7 drosophila
932	105	6.2	4117	2	08IRV9	08irv9 drosophila
933	105	6.2	4179	2	09WAY4	09way4 drosophila
934	105	6.2	4223	2	08MRN3	08mrn3 drosophila
935	105	6.2	4228	2	08IRV8	08irv8 drosophila
936	105	6.2	4816	2	08T103	08t103 bombyx mori
937	104.5	6.2	265	2	002280	002280 caenorhabdi
938	104.5	6.2	360	2	08MR6	08mr6 drosophila
939	104.5	6.2	365	2	08BXJ7	08bxj7 m mus muscu
940	104.5	6.2	395	2	08BZP4	08bzp4 mus musculus
941	104.5	6.2	417	1	FVR_CERAE	P32506 cercopithec
942	104.5	6.2	430	2	08N4F1	08n4f1 homo sapien
943	104.5	6.2	431	2	AAQ88508	Aa88508 homo sapi
944	104.5	6.2	523	2	08K2H7	08k2h7 mus musculus
945	104.5	6.2	538	2	09OXO7	09oxy7 bos taurus
946	104.5	6.2	582	2	09SNZ5	09snz5 bos taurus
947	104.5	6.2	722	2	06GNB3	06gnb3 xenopus lae
948	104.5	6.2	920	2	09P232	09p232 homo sapien
949	104.5	6.2	931	2	06KAM5	06kam5 mus musculus
950	104.5	6.2	931	2	BAD21432	Bad21432 mus muscu
951	104.5	6.2	1184	2	075339	075339 homo sapien
952	104.5	6.2	1184	2	06TW99	06tw99 homo sapien
953	104.5	6.2	1184	2	AAQ89263	Aa89263 homo sapi
954	104.5	6.2	1185	2	07PRK4	07prk4 anopheles g
955	104.5	6.2	1377	1	NEO1_HUMAN	P97603 rattus norv
956	104.5	6.2	1461	1	NEO1_HUMAN	092859 homo sapien
957	104.5	6.2	2222	2	097354	097354 drosophila
958	104.5	6.2	2230	2	08B67	08b67 drosophila
959	104.5	6.2	2230	2	AAQ09028	Aa09028 drosophila
960	104	6.2	299	1	ALC_RABIT	P01879 cyctolagus
961	104	6.2	307	2	054547	054547 rattus norv
962	104	6.2	307	2	AAH61820	Aah61820 rattus no
963	104	6.2	334	2	09NR44	09nr44 homo sapien
964	104	6.2	404	2	08BYP1	08byp1 mus musculus
965	104	6.2	524	1	BUTY_MOUSE	Q62556 mus musculus
966	104	6.2	524	2	0921K7	0921k7 mus musculus
967	104	6.2	600	2	08NTW7	08ntw7 homo sapien
968	104	6.2	620	2	06IGJ3	06igj3 drosophila
969	104	6.2	694	2	08SWT7	08swt7 drosophila
970	104	6.2	740	2	096F29	096f29 homo sapien
971	104	6.2	789	2	06X936	06x936 rattus norv
972	104	6.2	789	2	AAQ78673	Aa78673 rattus no
973	104	6.2	800	2	07TS18	07ts18 mus musculus
974	104	6.2	801	1	FGR3_MOUSE	061851 mus musculus
975	104	6.2	868	1	MUSK_MOUSE	061006 mus musculus
976	104	6.2	998	2	09K4T6	09k4t6 drosophila
977	104	6.2	1099	2	07TMR8	07tmr8 mus musculus
978	104	6.2	1503	2	08T4L8	08t4l8 drosophila
979	103.5	6.1	147	2	08CFJ3	08cfj3 mus musculus
980	103.5	6.1	275	2	09BDN9	09bdn9 papio anubi

981	103.5	6.1	280	2	Q8UWK1	Q8uwl1 ictalurus p	1054	102	6.0	702	1	CEA5_HUMAN	P06731 homo sapien
982	103.5	6.1	287	2	Q9QW80	Q9qwr0 mus sp. . f	1055	102	6.0	702	2	Q8N4D0	Q8n4d0 homo sapien
983	103.5	6.1	329	2	BAC26992	Bac26992 mus muscu	1056	102	6.0	800	2	Q99052	Q99052 mus musculus
984	103.5	6.1	356	1	HP1L_MOUSE	Q9qpw8 mus sp. . f	1057	102	6.0	1030	2	Q8NFA8	Q8nfa8 homo sapien
985	103.5	6.1	376	2	Q9QW78	Q9qwr78 mus sp. . f	1058	102	6.0	1032	2	Q8NFA8	Q8nfa8 homo sapien
986	103.5	6.1	388	2	Q8NC34	Q8nc34 homo sapien	1059	102	6.0	1038	2	Q8AXZ4	Q8axz4 brachydanto
987	103.5	6.1	534	2	Q8NBI8	Q8nbi8 homo sapien	1060	102	6.0	1098	2	Q961D6	Q961d6 drosophila
988	103.5	6.1	544	2	Q8NBI8	Q8nbi8 homo sapien	1061	102	6.0	1249	2	Q7TMZ9	Q7tmz9 ratuus norv
989	103.5	6.1	601	2	Q96CJ3	Q96cj3 homo sapien	1062	102	6.0	1371	1	MYPC_CHICK	Q96c8 gallus gall
990	103.5	6.1	628	1	LI_HUMAN	P50895 homo sapien	1063	102	6.0	1332	2	Q9VOW7	Q9vow7 drosophila
991	103.5	6.1	628	2	Q86VC7	Q86vc7 homo sapien	1064	102	6.0	1332	2	Q9BN17	Q9bn17 drosophila
992	103.5	6.1	677	1	NRG1_XENLA	Q93383 xenopus lae	1065	102	6.0	1426	2	Q8Z2T1	Q8z2t1 enterococcu
993	103.5	6.1	799	2	Q8C3V5	Q8c3v5 mus musculus	1066	101.5	6.0	336	1	Q226_MACMU	Q18906 macaca mula
994	103.5	6.1	799	2	Q8CIB8	Q8cib8 mus musculus	1067	101.5	6.0	413	2	Q26438	Q26438 hyalophora
995	103.5	6.1	819	1	FGRI_CHICK	P21804 gallus gall	1068	101.5	6.0	417	1	PVR_HUMAN	P15151 homo sapien
996	103.5	6.1	824	2	Q912B6	Q912b6 pleurodeles	1069	101.5	6.0	417	2	Q96EJ1	Q96ej1 homo sapien
997	103.5	6.1	940	2	Q8NFA7	Q8nfa7 homo sapien	1070	101.5	6.0	606	2	Q9VME6	Q9vme6 drosophila
998	103.5	6.1	958	2	Q9SR27	Q9sr27 drosophila	1071	101.5	6.0	629	2	Q9BS86	Q9bs86 ratuus norv
999	103.5	6.1	1356	1	VGR2_HUMAN	P35968 homo sapien	1072	101.5	6.0	634	2	Q96P30	Q96p30 homo sapien
1000	103.5	6.1	1513	2	Q90270	Q90270 brachydanto	1073	101.5	6.0	686	1	SILB_HUMAN	Q96r16 homo sapien
1001	103.5	6.1	1612	1	ROB1_MOUSE	Q89026 mus musculus	1074	101.5	6.0	802	2	Q8TDA0	Q8tda0 homo sapien
1002	103.5	6.1	1651	1	ROB1_HUMAN	Q9y6n7 homo sapien	1075	101.5	6.0	829	2	Q9PSV8	Q9psv8 xenopus lae
1003	103	6.1	7105	2	Q7PXW9	Q7pxw9 anopheles g	1076	101.5	6.0	898	1	FAS2_SCHAM	P22648 schistocerc
1004	103	6.1	229	2	Q7PUC4	Q7puc4 anopheles g	1077	101.5	6.0	912	1	TCAS_RABIT	Q28730 oryctolagus
1005	103	6.1	415	2	Q60977	Q60977 mus musculus	1078	101.5	6.0	1194	2	Q7TPV3	Q7tpv3 mus musculus
1006	103	6.1	498	2	Q8BRT6	Q8brr6 mus musculus	1079	101.5	6.0	1214	2	Q6ZQA6	Q6zqa6 mus musculus
1007	103	6.1	518	2	BAC38136	Bac38136 mus muscu	1080	101.5	6.0	1250	2	Q8BV01	Q8bv01 mus muscu
1008	103	6.1	583	2	Q7ZSP1	Q7zsp1 homo sapien	1081	101.5	6.0	1260	1	CAML_MOUSE	P11627 mus musculus
1009	103	6.1	606	2	Q6IRH8	Q6irh8 ratuus norv	1082	101	6.0	298	2	Q9GLT4	Q9gl74 cetopithec
1010	103	6.1	606	2	AAH70916	AAH70916 ratuus no	1083	101	6.0	300	2	Q8BEK0	Q8bek0 compox viru
1011	103	6.1	702	2	Q8OW67	Q8ow67 ratuus norv	1084	101	6.0	507	2	Q96K90	Q96k90 homo sapien
1012	103	6.1	708	2	Q6UWL6	Q6uwl6 homo sapien	1085	101	6.0	584	2	Q90989	Q90989 gallus gall
1013	103	6.1	708	2	AA089102	AA089102 homo sapi	1086	101	6.0	605	2	Q8RTU0	Q8rtu0 homo sapien
1014	103	6.1	763	2	Q95YM9	Q95ym9 halocynthia	1087	101	6.0	606	2	Q8CTJ4	Q8ctj4 mus musculus
1015	103	6.1	873	1	FAST_DROME	FA27285 drosophil	1088	101	6.0	620	1	SNP_COTUA	Q92154 coturnix co
1016	103	6.1	986	2	Q6DGI7	Q6dgi7 brachydanto	1089	101	6.0	626	2	Q90880	Q90880 gallus gall
1017	103	6.1	1388	2	Q7QKD0	Q7qkd0 anopheles g	1090	101	6.0	673	2	Q6MZW2	Q6mzw2 homo sapien
1018	103	6.1	1470	1	ROB2_MOUSE	Q7tpd3 mus musculus	1091	101	6.0	673	2	CAE45915	Q9upui1 homo sapi
1019	103	6.1	2693	2	Q8ISF3	Q8isf3 caenorhabdi	1092	101	6.0	693	2	Q9JPU1	Q9jpu1 homo sapien
1020	103	6.1	2708	2	Q8ISF4	Q8isf4 caenorhabdi	1093	101	6.0	700	2	Q7NSU7	Q7nsu7 mus musculus
1021	103	6.1	2808	2	Q8MNS1	Q8mns1 caenorhabdi	1094	101	6.0	700	2	BAC33658	Bac33658 m es cell
1022	103	6.1	2808	2	Q8MNS0	Q8mns0 caenorhabdi	1095	101	6.0	743	2	Q6P1M7	Q6p1m7 homo sapien
1023	103	6.1	18519	2	Q8ISF6	Q8isf6 caenorhabdi	1096	101	6.0	743	2	AAH11846	AAH11846 homo sapi
1024	103	6.1	18534	2	Q8ISF7	Q8isf7 caenorhabdi	1097	101	6.0	743	2	AAH64986	AAH64986 homo sapi
1025	102.5	6.1	318	2	Q8BBI6	Q8bbi6 variola vir	1098	101	6.0	789	2	Q80W68	Q80w68 mus musculus
1026	102.5	6.1	318	2	Q9QNG4	Q9qng4 variola min	1099	101	6.0	796	2	Q91287	Q91287 pleurodeles
1027	102.5	6.1	354	1	HP1L_RAT	P03994 ratuus norv	1100	101	6.0	890	1	TYO3_HUMAN	Q96t18 homo sapien
1028	102.5	6.1	356	2	Q8BCK2	Q8bck2 brachylosto	1101	101	6.0	894	1	Q8EVR3	Q8evr3 homo sapien
1029	102.5	6.1	399	2	Q7QCH7	Q7qch7 anopheles g	1102	101	6.0	990	2	MERRK_RAT	P57097 ratuus norv
1030	102.5	6.1	413	2	Q27418	Q27418 manduca sex	1103	101	6.0	1214	2	Q24463	Q24463 homo sapien
1031	102.5	6.1	662	2	Q60926	Q60926 homo sapien	1104	101	6.0	1742	2	Q24463	Q24463 homo sapien
1032	102.5	6.1	992	2	Q9C0L5	Q9c0l5 homo sapien	1105	101	6.0	6048	2	Q7ZN85	Q7zn85 caenorhabdi
1033	102.5	6.1	1176	1	KMLS_BOVIN	Q28824 bos taurus	1106	101	6.0	6839	2	Q23550	Q23550 caenorhabdi
1034	102.5	6.1	1184	2	Q81Y15	Q81y15 homo sapien	1107	101	6.0	6839	2	CAA98064	CAA98064 caenorhab
1035	102.5	6.1	1651	1	ROB1_RAT	Q55005 ratuus norv	1108	101	6.0	7158	2	CAA98081	CAA98081 caenorhab
1036	102	6.0	305	2	Q6ZS95	Q6z995 homo sapien	1109	101	6.0	7158	2	Q23551	Q23551 caenorhabdi
1037	102	6.0	305	2	BAC87059	Bac87059 homo sapi	1110	100.5	6.0	280	2	Q8UW11	Q8uw11 ictalurus p
1038	102	6.0	314	2	Q8BCK8	Q8bck8 vaccinia vi	1111	100.5	6.0	323	2	Q9EDM9	Q9edm9 macaca neme
1039	102	6.0	319	2	Q00477	Q00477 homo sapien	1112	100.5	6.0	333	2	Q90Z41	Q90z41 gallus gall
1040	102	6.0	332	2	Q9BU81	Q9bu81 homo sapien	1113	100.5	6.0	608	2	Q9EPFL	Q9epfl mus musculus
1041	102	6.0	332	2	Q8TA95	Q8ta95 homo sapien	1114	100.5	6.0	700	1	MEBP_HUMAN	Q16820 homo sapien
1042	102	6.0	332	2	AAH02832	AAH02832 homo sapien	1121	100.5	6.0	802	1	FGR4_HUMAN	P22455 homo sapien
1043	102	6.0	332	2	AAH20214	Aah20214 homo sapi	1122	100.5	6.0	847	2	Q8BCA1	Q8bc41 shewanella
1044	102	6.0	334	2	Q76PA0	Q76pa0 homo sapien	1123	100.5	6.0	847	1	CD22_HUMAN	P20273 homo sapien
1045	102	6.0	350	2	Q8MS24	Q8ms24 drosophila	1124	100.5	6.0	906	2	Q8TPY9	Q8tpy9 methanosarc
1046	102	6.0	357	2	Q1S338	Q1s338 homo sapien	1125	100.5	6.0	1250	2	Q88971	Q88971 mus musculus
1047	102	6.0	359	2	P78410	P78410 homo sapien	1126	100	5.9	307	2	Q94431	Q94431 ciona intes
1048	102	6.0	504	2	Q6NNA1	Q6nnai drosophila							
1049	102	6.0	504	2	AAH96184	AAH96184 drosophila							
1050	102	6.0	508	2	Q9VGD2	Q9vgd2 drosophila							
1051	102	6.0	605	2	Q96084	Q96084 homo sapien							
1052	102	6.0	626	1	MAG_MOUSE	P20917 mus musculus							
1053	102	6.0	664	2	Q9VGD3	Q9vgd3 drosophila							

1127	100	5.9	314	2	OB8BK7	OB8bk7 vaccinia vi	1200	98.5	5.8	285	2	Q7ZYX30	Q7zyx30 xenopus lae
1128	100	5.9	322	1	ICOL_MOUSE	Q9j1h8 mus musculu	1201	98.5	5.8	288	2	Q22385	Q22385 caenorhabd1
1129	100	5.9	322	1	BAC30938	Bac30938 mus,muscu	1202	98.5	5.8	289	2	Q9YN57	Q9yn57 vaccinia vi
1130	100	5.9	354	1	HPL1_HUMAN	P10915 homo sapien	1203	98.5	5.8	309	2	Q9YN57	Q9yn57 vaccinia vi
1131	100	5.9	404	2	OB8LQ9	OB8lq9 mus musculu	1204	98.5	5.8	316	2	Q7Q0P9	Q7q0p9 anophelies g
1132	100	5.9	458	1	CD4_PANTR	P16004 pan troglod	1205	98.5	5.8	327	2	Q6PCB8	Q6pcb8 homo sapien
1133	100	5.9	504	2	Q989Z3	Q989z3 gallus gall	1206	98.5	5.8	327	2	AAH59398	Aah59398 homo sapi
1134	100	5.9	527	2	BAC32687	Bac32687 mus muscu	1207	98.5	5.8	413	1	HEMO_MANSE	P11398 manduca sex
1135	100	5.9	584	2	Q989Z1	Q989z1 gallus gall	1208	98.5	5.8	482	2	Q741A5	Q741a5 mycobacteri
1136	100	5.9	592	2	Q9JLNS	Q9jlns mus musculu	1209	98.5	5.8	482	2	AA803504	Aa803504 mycobacte
1137	100	5.9	626	2	Q989Z2	Q989z2 gallus gall	1210	98.5	5.8	493	2	Q6P5Y4	Q6p5y4 homo sapien
1138	100	5.9	684	2	Q7SRG1	Q7srg1 neurospora	1211	98.5	5.8	525	2	Q7QJK5	Q7qjk5 anophelies g
1139	100	5.9	784	2	OB10G3	OB10g3 drosophila	1212	98.5	5.8	548	2	Q921J3	Q921j3 rattus norv
1140	100	5.9	807	2	Q6DD66	Q6dd66 xenopus lae	1213	98.5	5.8	602	2	NRG1_CHICK	NRG1 chick
1141	100	5.9	818	1	TRKB_CHICK	Q91987 gallus gall	1214	98.5	5.8	611	2	Q8CTC7	Q8ctc7 streptococc
1142	100	5.9	818	1	Q9PSV9	Q9psv9 xenopus lae	1215	98.5	5.8	648	2	Q8R2Y2	Q8r2y2 mus musculu
1143	100	5.9	846	2	Q57577	Q57577 cynops pyrr	1216	98.5	5.8	1005	2	P799Z1	P799z1 xenopus lae
1144	100	5.9	1026	2	Q94780	Q94780 homo sapien	1217	98.5	5.8	1014	2	Q8NFA6	Q8nfa6 homo sapien
1145	100	5.9	1100	2	Q94779	Q94779 homo sapien	1218	98.5	5.8	1021	2	P79757	P79757 gallus gall
1146	100	5.9	1100	2	Q57576	Q57576 cynops pyrr	1219	98.5	5.8	1333	1	VGRI_MOUSE	Vgri mouse
1147	100	5.9	1180	2	Q8TJ57	Q8tj57 methanocarc	1220	98	5.8	229	2	Q7Q8G3	Q7q8g3
1148	99.5	5.9	295	2	Q9GL75	Q9gl75 bos taurus	1221	98	5.8	347	2	Q9H730	Q9h730
1149	99.5	5.9	323	2	Q9BDM4	Q9bdm4 macaca mula	1222	98	5.8	347	2	Q9H730	Q9h730
1150	99.5	5.9	416	2	Q96360	Q96360 hyphantria	1223	98	5.8	394	2	Q8HXK9	Q8hxr9
1151	99.5	5.9	432	2	Q6DD87	Q6dd87 xenopus lae	1224	98	5.8	413	2	Q8BGH4	Q8bgh4 macaca mula
1152	99.5	5.9	459	1	CD4_RABIT	P46630 coryctolagus	1225	98	5.8	443	2	Q8N2F4	Q8n2f4 homo sapien
1153	99.5	5.9	549	2	Q6PFC5	Q6pfc5 mus musculu	1226	98	5.8	500	2	Q6UX41	Q6ux41 homo sapien
1154	99.5	5.9	549	2	AAH57628	Aah57628 mus muscu	1227	98	5.8	500	2	AAQ88887	Aa888887 homo sapi
1155	99.5	5.9	549	2	BAC31895	Bac31895 m adult r	1228	98	5.8	589	2	Q8R366	Q8r366 mus musculu
1156	99.5	5.9	549	2	BAC32002	Bac32002 m adult r	1229	98	5.8	640	2	Q8BGH8	Q8bgh8 m mus muscu
1157	99.5	5.9	626	1	MAG_HUMAN	P20916 homo sapien	1230	98	5.8	640	2	Q8C031	Q8c031 mus musculu
1158	99.5	5.9	876	2	Q7PF78	Q7pf78 anophelies g	1231	98	5.8	697	1	SILA_HUMAN	Sila human
1159	99.5	5.9	1009	2	Q93250	Q93250 xenopus lae	1232	98	5.8	847	2	Q8N475	Q8n475
1160	99.5	5.9	1019	2	Q8BJK6	Q8bjk6 mus musculu	1233	98	5.8	850	2	Q9ULF7	Q9ulf7
1161	99.5	5.9	1028	2	Q62682	Q62682 rattus norv	1234	98	5.8	880	1	TYO3_MOUSE	Ty03 mouse
1162	99.5	5.9	1031	2	Q8OYX7	Q8oyx7 mus musculu	1235	98	5.8	880	2	Q6NZM6	Q6nzm6
1163	99.5	5.9	1256	2	Q9JTX1	Q9jtx1 mus musculu	1236	98	5.8	880	2	Q6NZM6	Q6nzm6
1164	99.5	5.9	1379	2	P79701	P79701 cecurini x co	1237	98	5.8	880	2	AAH60508	Aah60508 mus muscu
1165	99.5	5.9	1450	2	Q7QCP2	Q7qcp2 anophelies g	1238	98	5.8	931	2	Q7T2Z5	Q7t2z5 gallus gall
1166	99.5	5.9	1450	2	Q6PACO	Q6pac0 mus musculu	1239	98	5.8	939	2	Q9VH85	Q9vh85 drosophila
1167	99.5	5.9	1569	2	AAH60378	Aah60378 mus muscu	1240	98	5.8	945	2	Q77589	Q77589 equus cabal
1168	99.5	5.9	1666	1	MYM1_MOUSE	Q62234 mus musculu	1241	98	5.8	1021	2	Q93033	Q93033 homo sapien
1169	99.5	5.9	1666	2	CAB4F494	Cab4f494 mus muscu	1242	98	5.8	1252	2	Q9JL11	Q9jl11
1170	99	5.9	234	2	Q8T2Q9	Q8t2q9 homo sapien	1243	98	5.8	1489	2	Q90815	Q90815 gallus gall
1171	99	5.9	275	1	V055_FOWPV	P21975 fowlpox vir	1244	98	5.8	1896	2	Q91A11	Q91a11 xenopus lae
1172	99	5.9	275	2	Q70H96	Q70h96 fowlpox vir	1245	97.5	5.8	210	2	Q7PVL9	Q7pvl9 anophelies g
1173	99	5.9	275	2	CAE52600	Ca52600 fowlpox v	1246	97.5	5.8	257	2	Q6NW92	Q6nw92 brachydanio
1174	99	5.9	313	2	Q89197	Q89197 variola vir	1247	97.5	5.8	257	2	AAH67677	Aah67677 brachydan
1175	99	5.9	359	1	HPL3_MOUSE	Q80478 mus musculu	1248	97.5	5.8	261	2	Q9W6V1	Q9w6v1 gallus gall
1176	99	5.9	458	1	CD4_HUMAN	P01730 homo sapien	1249	97.5	5.8	262	2	Q80T70	Q80t70 mus musculu
1177	99	5.9	478	2	BAC35000	Bac35000 m 13 days	1250	97.5	5.8	313	2	Q90Z91	Q90z91
1178	99	5.9	520	2	Q7Z3M6	Q7z3m6 homo sapien	1251	97.5	5.8	316	2	Q8BBK1	Q8bbk1 brachydanio
1179	99	5.9	542	2	Q8NHN5	Q8nhn5 homo sapien	1252	97.5	5.8	354	1	HPL1_BOVIN	Hpl1 bovin
1180	99	5.9	584	2	Q800478	Q800478 homo sapien	1253	97.5	5.8	354	1	HPL1_PIG	Hpl1 pig
1181	99	5.9	633	2	Q7Z5P2	Q7z5p2 homo sapien	1254	97.5	5.8	418	2	Q9EPN5	Q9epn5
1182	99	5.9	734	2	Q96LH4	Q96lha homo sapien	1255	97.5	5.8	423	2	Q9WRU4	Q9wru4
1183	99	5.9	734	2	Q96EJ3	Q96ej3 homo sapien	1256	97.5	5.8	457	1	CD4_SAISC	CD4 saisc
1184	99	5.9	742	2	Q8N6S2	Q8n6s2 homo sapien	1257	97.5	5.8	457	1	Q8H2T7	Q8h2t7
1185	99	5.9	756	2	Q800Z0	Q800z0 brachydanio	1258	97.5	5.8	473	2	Q83HS2	Q83hs2 tropheryma
1186	99	5.9	773	2	Q9NSW7	Q9nsw7 homo sapien	1259	97.5	5.8	473	2	Q83MX5	Q83mx5
1187	99	5.9	789	2	Q8CJ59	Q8cj59 mus musculu	1260	97.5	5.8	476	2	Q80WU0	Q80wu0
1188	99	5.9	812	1	FERRI_XENLA	P22182 xenopus lae	1261	97.5	5.8	510	2	Q6EH12	Q6eh12 rattus norv
1189	99	5.9	818	2	Q91742	Q91742 xenopus lae	1262	97.5	5.8	534	2	Q86SE4	Q86se4 homo sapien
1190	99	5.9	831	2	Q718Y9	Q718y9 gallus gall	1263	97.5	5.8	534	2	Q86ET2	Q86et2 pan troglod
1191	99	5.9	831	2	AAQ14282	Aaq14282 gallus ga	1264	97.5	5.8	764	1	ICCR_DROME	ICCR drome
1192	99	5.9	862	1	CD22_MOUSE	P25329 mus musculu	1265	97.5	5.8	764	2	Q8MOQ1	Q8mq01 drosophila
1193	99	5.9	997	2	Q7PXF0	Q7pxf0 anophelies g	1266	97.5	5.8	764	2	Q9W4U1	Q9w4u1 drosophila
1194	99	5.9	1011	2	BAC32470	Bac32470 m adult m	1267	97.5	5.8	821	1	TRK3_MOUSE	Trk3 mouse
1195	99	5.9	1375	2	Q94537	Q94537 drosophila	1268	97.5	5.8	876	1	Q78E87	Q78e87 mus musculu
1196	99	5.9	1526	2	Q94538	Q94538 drosophila	1269	97.5	5.8	931	2	Q95185	Q95185 homo sapien
1197	99	5.9	3197	2	Q9WID5	Q9wid5 drosophila	1270	97.5	5.8	1348	2	Q8YA37	Q8ya37 listeria mo
1198	98.5	5.8	279	2	Q9UD50	Q9ud50 homo sapien	1271	97.5	5.8	1443	1	NEO1_CHICK	Neo1 chick
1199	98.5	5.8	283	2	Q7QGR4	Q7qgr4 anophelies g	1272	97	5.7	240	2	Q8WUK3	Q8wuk3 homo sapien

1273	97	5.7	279	2	Q7TST0	Q7tst0 mus musculu	1346	96	5.7	612	2	Q8BGQ5	Q8bgq5 m mus muscu
1274	97	5.7	280	2	Q8UW12	Q8uw12 ictalurus p	1347	96	5.7	619	2	Q7PX10	Q7px10 anopheles g
1275	97	5.7	304	2	Q9BE26	Q9be26 macaca fasc	1348	96	5.7	636	2	Q7PX03	Q7px03 homo sapien
1276	97	5.7	305	2	Q7PR66	Q7pr66 anopheles g	1349	96	5.7	636	2	AAH41374	Aah41374 homo sapi
1277	97	5.7	307	2	Q66607	Q66607 equid herpe	1350	96	5.7	639	1	NRG1_HUMAN	Q02297 h pro-neure
1278	97	5.7	310	2	Q6BB18	Q6be18 vaccinia vl	1351	96	5.7	640	2	Q7RTV8	Q7rtv8 homo sapien
1279	97	5.7	317	2	Q8BER2	Q8ber2 compox viru	1352	96	5.7	640	2	Q9HCJ2	Q9hcj2 homo sapien
1280	97	5.7	333	2	Q8HXK8	Q8hxr8 cercopitheci	1353	96	5.7	640	2	AAQ86660	Aaq86660 homo sapi
1281	97	5.7	456	1	Q7PUM9	Q7pum9 anopheles g	1354	96	5.7	650	1	LIB1_HUMAN	Q8n16 h leukocyte
1282	97	5.7	485	2	A1BG_HUMAN	P04217 homo sapien	1355	96	5.7	739	1	VCAL_MOUSE	P29533 mus musculu
1283	97	5.7	637	2	Q8TC35	Q8tc35 homo sapien	1356	96	5.7	739	1	Q91X38	Q91x38 mus musculu
1284	97	5.7	724	2	Q8MXU5	Q8mxu5 caenorhabdi	1357	96	5.7	766	2	Q810H3	Q810h3 mus musculu
1285	97	5.7	739	1	VCAL_HUMAN	P19320 homo sapien	1358	96	5.7	802	2	Q95M13	Q95m13 bos taurus
1286	97	5.7	739	2	Q6NUP8	Q6nup8 homo sapien	1359	96	5.7	1016	2	Q7JFL6	Q7jfl6 oryctolagus
1287	97	5.7	751	2	Q39294	Q39294 equine herp	1360	96	5.7	1145	2	Q9BKL8	Q9bkl8 alysiia cal
1288	97	5.7	778	2	AAH68490	Aah68490 homo sapi	1361	96	5.7	1193	2	Q9YQW1	Q9yqw1 drosophila
1289	97	5.7	824	2	Q90749	Q90749 gallus gall	1362	96	5.7	1252	2	Q9E0S9	Q9eqs9 mus musculu
1290	97	5.7	931	2	Q8NF26	Q8nf26 homo sapien	1363	96	5.7	1253	2	Q9E0S8	Q9eqs8 mus musculu
1291	97	5.7	949	1	MDCL_RAT	P60756 rattus norv	1364	96	5.7	1294	2	Q80TB0	Q80tb0 mus musculu
1292	97	5.7	1028	2	Q07409	Q07409 mus musculu	1365	96	5.7	1330	2	Q8Y479	Q8y479 listeria mo
1293	97	5.7	1147	1	KMLS_RABIT	P29284 oryctolagus	1366	96	5.7	1744	2	Q82YW8	Q82yw8 enterococcu
1294	97	5.7	1273	2	Q6R2F7	Q6r2f7 homo sapien	1367	96	5.7	6875	2	Q28733	Q28733 oryctolagus
1295	97	5.7	1273	2	AAH89909	Aah89909 homo sapi	1368	95.5	5.7	220	2	Q7PX67	Q7px67 anopheles g
1296	97	5.7	1274	1	MYPC_HUMAN	Q14836 homo sapien	1369	95.5	5.7	243	1	CD48_HUMAN	P09326 homo sapien
1297	97	5.7	1274	2	Q9UM53	Q9um53 homo sapien	1370	95.5	5.7	243	2	Q61A22	Q61a22 homo sapien
1298	97	5.7	1345	2	Q8VCD0	Q8vcd0 mus musculu	1371	95.5	5.7	308	2	CAG33293	Cag33293 homo sapi
1299	97	5.7	1367	1	VGR2_MOUSE	P35918 mus musculu	1372	95.5	5.7	308	2	Q6GVZ1	Q6gvz1 aracetaba v
1300	97	5.7	1535	2	Q23931	Q23931 drosophila	1373	95.5	5.7	308	2	Q91ZR9	Q91zr9 caratagalo o
1301	97	5.7	1860	2	Q7POF4	Q7pof4 anopheles g	1374	95.5	5.7	308	2	AAQ09951	Aaq09951 aracetaba
1302	97	5.7	6620	2	Q96AA2	Q96aa2 homo sapien	1375	95.5	5.7	416	2	Q9NPPE	Q9nppe homo sapien
1303	96.5	5.7	187	2	Q8K4B4	Q8k4e4 mus musculu	1376	95.5	5.7	611	2	Q9H9N1	Q9h9n1 homo sapien
1304	96.5	5.7	193	2	Q7QGT6	Q7qgt6 anopheles g	1377	95.5	5.7	611	2	Q7QW31	Q7qw32 oncorhynch
1305	96.5	5.7	313	2	Q85400	Q85400 variola maj	1378	95.5	5.7	692	2	CAD58653	Cad58653 oncorhyn
1306	96.5	5.7	332	2	Q8AYZ7	Q8ayz7 variola vit	1379	95.5	5.7	692	2	Q800Y9	Q800y9 brachydantio
1307	96.5	5.7	352	2	Q9K6V2	Q9k6v2 gallus gall	1380	95.5	5.7	757	2	Q7QCT0	Q7qct0 anopheles g
1308	96.5	5.7	385	2	Q9UQF5	Q9uqf5 homo sapien	1381	95.5	5.7	879	2	Q8VI99	Q8vi99 rattus norv
1309	96.5	5.7	404	2	Q9Y3E9	Q9y3e9 homo sapien	1382	95.5	5.7	888	2	Q8VIA0	Q8via0 rattus norv
1310	96.5	5.7	433	2	Q9J2M8	Q9j2m8 macaca mula	1383	95.5	5.7	891	2	Q8BRX1	Q8brx1 mus musculu
1311	96.5	5.7	510	2	Q7L3E0	Q7l3e0 homo sapien	1384	95.5	5.7	1131	1	MYPF_CHICK	P16419 gallus gall
1312	96.5	5.7	510	2	AAH13867	Aah13867 homo sapi	1385	95.5	5.7	1163	2	Q7XG19	Q7xg19 oryza sativ
1313	96.5	5.7	571	2	Q8SPI8	Q8spi8 sus scrofa	1386	95.5	5.7	1163	2	Q94HMS	Q94hms oryza sativ
1314	96.5	5.7	537	2	Q8IUT0	Q8iut0 homo sapien	1387	95.5	5.7	1242	1	NPEN_MOUSE	Q9qz87 mus musculu
1315	96.5	5.7	733	2	Q8SQ83	Q8sq83 trichoburus	1388	95.5	5.7	1264	1	P91767	P91767 manduca sex
1316	96.5	5.7	772	2	Q9Y2J6	Q9y2j6 homo sapien	1389	95.5	5.7	1948	1	PTNS_HUMAN	Q13332 homo sapien
1317	96.5	5.7	777	2	Q6P555	Q6p555 mus musculu	1390	95	5.6	181	2	Q916F5	Q916f5 xenopus lae
1318	96.5	5.7	777	2	AAH63072	Aah63072 mus muscu	1391	95	5.6	229	2	Q7PVL3	Q7pvl3 anopheles g
1319	96.5	5.7	778	2	Q8BR86	Q8br86 mus musculu	1392	95	5.6	252	2	Q9CX63	Q9cx63 mus musculu
1320	96.5	5.7	782	2	Q9BSA5	Q9bas5 rattus norv	1393	95	5.6	270	2	Q00426	Q00426 homo sapien
1321	96.5	5.7	800	2	Q86LPE9	Q86lpe9 drosophila	1394	95	5.6	312	2	Q8BBJ3	Q8bbj3 rabbitpox v
1322	96.5	5.7	801	2	Q86LPE8	Q86lpe8 drosophila	1395	95	5.6	438	2	Q920C3	Q920c3 mus musculu
1323	96.5	5.7	804	2	Q800Z1	Q800z1 brachydantio	1396	95	5.6	457	2	Q96OD1	Q96od1 drosophila
1324	96.5	5.7	806	2	Q90Z00	Q90z00 brachydantio	1397	95	5.6	521	1	C166_RABIT	Q46651 oryctolagus
1325	96.5	5.7	1200	1	HYAL_STRPU	Q76536 stronygloce	1398	95	5.6	591	2	Q9UQJ3	Q9uqj3 homo sapien
1326	96.5	5.7	1232	2	Q8TCC8	Q8tcg8 homo sapien	1399	95	5.6	601	2	Q86X29	Q86x29 homo sapien
1327	96.5	5.7	1560	1	TENN_MOUSE	Q80271 mus musculu	1400	95	5.6	814	2	Q81VU1	Q81vu1 homo sapien
1328	96.5	5.7	2013	2	Q8Y9T8	Q8y9t8 listeria mo	1401	95	5.6	814	2	Q91897	Q91897 xenopus lae
1329	96.5	5.7	3198	2	Q9U8G8	Q9u8g8 manduca sex	1402	95	5.6	814	2	AAH67107	Aah67107 homo sapi
1330	96	5.7	228	2	Q7PVK5	Q7pvk5 anopheles g	1403	95	5.6	847	2	Q8BPR2	Q8bpr2 m mus muscu
1331	96	5.7	224	2	Q9MCS7	Q9mc87 bacterioph	1404	95	5.6	847	2	Q8CAT3	Q8cat3 mus musculu
1332	96	5.7	236	2	Q6P5S3	Q6p5s3 homo sapien	1405	95	5.6	879	1	FPKP_MOUSE	Q9wv91 mus musculu
1333	96	5.7	236	2	AAH62711	Aah62711 homo sapi	1406	95	5.6	879	1	FPKP_RAT	Q6z786 rattus norv
1334	96	5.7	252	2	Q8ML12	Q8ml12 drosophila	1407	95	5.6	944	1	MDCL_MOUSE	P60755 mus musculu
1335	96	5.7	293	2	AAH38070	Aah38070 mus muscu	1408	95	5.6	994	1	MERR_MOUSE	Q60805 mus musculu
1336	96	5.7	310	2	Q7OK35	Q7ok35 anopheles g	1409	95	5.6	1052	2	Q7PMV4	Q7pmv4 drosophila
1337	96	5.7	310	2	Q7TQ98	Q7tq98 mus musculu	1410	95	5.6	1270	2	MYPC_MOUSE	Q70468 mus musculu
1338	96	5.7	310	2	Q8BB17	Q8be17 vaccinia vl	1411	95	5.6	1304	1	Q9VBES	Q9vbes drosophila
1339	96	5.7	312	2	Q8BBJ2	Q8bej2 rabbitpox v	1412	95	5.6	1371	2	Q8BV57	Q8bv57 mus musculu
1340	96	5.7	360	2	Q8N732	Q8n732 homo sapien	1413	95	5.6	1375	2	Q8W147	Q8w147 drosophila
1341	96	5.7	395	2	Q6IEF8	Q6ief8 paracitichth	1414	95	5.6	1450	1	MPSF_CHICK	Q02173 gallus gall
1342	96	5.7	407	1	G1C2_VIBCH	Q9klp4 vibrio chol	1415	95	5.6	1501	2	Q7RTT7	Q7rtt7 mus musculu
1343	96	5.7	462	2	Q7RTW1	Q7rtw1 homo sapien	1416	95	5.6	1501	2	Q9QM00	Q9qm00 rattus sp.
1344	96	5.7	492	2	Q7QD44	Q7qd44 anopheles g	1417	95	5.6	1526	2	Q9V6D5	Q9v6d5 drosophila
1345	96	5.7	570	2	Q6GM29	Q6gm29 xenopus lae	1418	95	5.6	1527	2	Q9V2Z4	Q9v2z4 drosophila


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1419 95 5 6 1863 2 064605 064605 rattus norv
1420 95 5 6 1898 2 09B017 09B017 mus musculu
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1423 95 5 6 22152 1 08Wx17 08Wx17 homo sapien
1424 94.5 5 6 315 1 HEMA VACC 08Wx17 vaccinia vi
1425 94.5 5 6 330 2 08C2T8 08C218 mus musculu
1426 94.5 5 6 341 2 0819K3 0819K3 branchiocto
1427 94.5 5 6 371 2 06DCN5 06DCN5 xenopus lae
1428 94.5 5 6 381 2 09Y4A4 09Y4A4 homo sapien
1429 94.5 5 6 388 2 08NFZ8 08NFZ8 homo sapien
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1434 94.5 5 6 570 2 06GLY1 06GLY1 xenopus lae
1435 94.5 5 6 588 1 C166 CHICK P42292 gallus gall
1436 94.5 5 6 593 2 06INM5 06INM5 xenopus lae
1437 94.5 5 6 593 2 AAH72253 AAH72253 xenopus l
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1440 94.5 5 6 755 2 08CCP8 08CCP8 mus musculu
1441 94.5 5 6 822 1 TRXB HUMAN Q16620 homo sapien
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1448 94.5 5 6 888 2 080YQ3 080YQ3 mus musculu
1449 94.5 5 6 891 2 090Y74 090Y74 mus musculu
1450 94.5 5 6 931 2 080747 080747 mus musculu
1451 94.5 5 6 930 2 08CD16 08CD16 mus musculu
1452 94.5 5 6 999 1 MERK HUMAN Q12866 homo sapien
1453 94.5 5 6 1083 2 076698 076698 caenorhabdi
1454 94.5 5 6 1256 2 035158 035158 rattus norv
1455 94.5 5 6 1327 2 080HL3 080HL3 gallus gall
1456 94 5 6 252 2 086P85 086P85 dtrosophila
1457 94 5 6 275 2 07PVW4 07PVW4 anopheles g
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1459 94 5 6 313 2 08BH36 08BH36 mesocricetu
1460 94 5 6 313 1 HEMA VARV P31807 variola vir
1461 94 5 6 313 2 035531 035531 rattus norv
1462 94 5 6 313 2 08AIV3 08AIV3 variola vir
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1474 94 5 6 583 2 08VZK7 08VZK7 arabidopsis
1475 94 5 6 602 2 09VFD9 09VFD9 arabidopsis
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1477 94 5 6 821 2 08BF70 08BF70 m mus muscu
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1479 94 5 6 887 2 08WY17 08WY17 anabaena sp
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1481 94 5 6 1010 1 CONT CHICK P41481 gallus gall
1482 94 5 6 1280 2 09EPX2 09EPX2 mus musculu
1483 94 5 6 1325 1 YDER ECOLI P32051 escherichia
1484 94 5 6 1343 1 VGR2 RAT 08J775 rattus norv
1485 94 5 6 1406 2 09GPF7 09GPF7 dtrosophila
1486 94 5 6 1463 2 09V008 09V008 dtrosophila
1487 94 5 6 1945 2 09V491 09V491 dtrosophila
1488 93.5 5 5 259 2 08UVAS 08UVAS brachydanio
1489 93.5 5 5 261 2 08AU04 08AU04 brachydanio
1490 93.5 5 5 296 2 042404 042404 gallus gall
1491 93.5 5 5 313 2 08UV33 08UV33 brachydanio
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1492 93.5 5 5 315 2 06UN41 06UN41 compox viru
1493 93.5 5 5 315 2 AAQ73184 AAQ73184 compox vi
1494 93.5 5 5 315 2 AAQ73183 AAQ73183 compox vi
1495 93.5 5 5 326 2 08UV70 08UV70 brachydanio
1496 93.5 5 5 329 1 CD86 HUMAN P42081 homo sapien
1497 93.5 5 5 329 2 AAH40261 AAH40261 homo sapi
1498 93.5 5 5 379 2 09CWM1 09CWM1 mus musculu
1499 93.5 5 5 388 2 08R464 08R464 mus musculu
1500 93.5 5 5 392 2 0923L4 0923L4 mus musculu

ALIGNMENTS
Query Match 100.0%; Score 1688; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-125;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGILLGLLLGHLTVPTDYGRILEVPEVSYGPKKGDVNLPCYDPLQGYQTVYVKMLVOR 60
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DB 61 GSDPVTIFLRSDSGDHIQQAQYQGRLLVSHKRGVDVSLQSTLEMDRSHYTCVWTQPT 120
QY 121 DGNQVVRDKTTERVQKLSKRPVTTGSGYGTTVQGMKISLQCCARGSPPISTYMYKQ 180
DB 121 DGNQVVRDKTTERVQKLSKRPVTTGSGYGTTVQGMKISLQCCARGSPPISTYMYKQ 180
QY 181 QTNNOEPIKAVATSTLLFKPAVIAADSGSYFCTAKGQVGSQHSQSDIYFVVKDSSKLKTK 240
DB 181 QTNNOEPIKAVATSTLLFKPAVIAADSGSYFCTAKGQVGSQHSQSDIYFVVKDSSKLKTK 240
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Db 181 QTNNOEBIKVATLSTLLFKPAVIADSGSYECTAKGVSGSEOHSDIVKFWKDSKLLKTK 240
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 Db 241 TEAPTMTYPLKATSTVKOSMDWTMDGYLGSTAGPKSLPVPAILIILISLCMVVFT 300
 QY 301 MAYIMLCRKTSQOEHYEYEAAR 321
 Db 301 MAYIMLCRKTSQOEHYEYEAAR 321

RESULT 2

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 ID AA088707; AA088707;
 AC AA088707; (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE STIGMA.
 GN UNQ317.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12975309;
 RA Clark H.F., Gunney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
 Raton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshgiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,
 RA Vanden R., Watanabe C., Wiesend D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.,
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 RT Bioinformatics Assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL: AY358341; AA088707.1; -.
 SQ SEQUENCE 321 AA; 35544 MW; B2AB2E315ID39C6E CRC64;

Query Match 100.0%; Score 1688; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1,3e-125;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHLYVDYGRPILEVPEBSVTGPKGDNVLPCTYDPLQGYTVLVKMLVOR 60
 Db 1 MGILLGLLLGLHLYVDYGRPILEVPEBSVTGPKGDNVLPCTYDPLQGYTVLVKMLVOR 60
 QY 61 GSDPVTITFLRDSGGHIOQAQKYGRLVSHKVPDVSLOLSTLEMDRSHYTCETWQTP 120
 Db 61 GSDPVTITFLRDSGGHIOQAQKYGRLVSHKVPDVSLOLSTLEMDRSHYTCETWQTP 120
 QY 121 DGNQVVRDKITELRVOKLVSKEPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180
 Db 121 DGNQVVRDKITELRVOKLVSKEPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180
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 Db 121 DGNQVVRDKITELRVOKLVSKEPTVTGSGYGFVTPQGRISLQCARSGSPISYIWKQ 180
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 QY 241 TEAPTMTYPLKATSTVKOSMDWTMDGYLGSTAGPKSLPVPAILIILISLCMVVFT 300
 Db 241 TEAPTMTYPLKATSTVKOSMDWTMDGYLGSTAGPKSLPVPAILIILISLCMVVFT 300
 QY 301 MAYIMLCRKTSQOEHYEYEAAR 321
 Db 301 MAYIMLCRKTSQOEHYEYEAAR 321

RESULT 3

Q9Y279 PRELIMINARY; PRT; 399 AA.
 ID Q9Y279; Q9Y279;
 AC Q9Y279; (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Z391g protein precursor (Ig superfamily protein).
 GN Name=Z391g; Synonyms=Z391G;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20461665; PubMed=11004523;
 RA Iarguane K., Colieux L., Kloos D.U., Fontes M., Wiesacker P.,
 RT "Cloning of Z391g, a novel gene with immunoglobulin-like domains
 RT located on human chromosome X.";
 RL Biochim. Biophys. Acta 1492:522-525 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywnicki M.I., Skalski U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Warr M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.,
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ13502; CAB51536.1; -.
 DR EMBL: BC010525; AAH0525.1; -.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR Pfam: PF00047; Ig2.
 DR SMART; SM00408; IGc2.1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 399 Z391g protein.
 SQ SEQUENCE 399 AA; 43987 MW; 735CA3BC58185035 CRC64;

Query Match 100.0%; Score 1688; DB 2; Length 399;
 Best Local Similarity 100.0%; Pred. No. 1,7e-125;
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 Db 61 GSDPVTITFLRDSGGHIOQAQKYGRLVSHKVPDVSLOLSTLEMDRSHYTCETWQTP 120
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Db 121 DGNQVVDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRSILQCGARSGSPISYIWKQ 180
Qy 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQGVSEHSDIVKRVVNDSSKLTXTK 240
Db 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQGVSEHSDIVKRVVNDSSKLTXTK 240
Qy 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLIISLCMVFT 300
Db 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLIISLCMVFT 300
Qy 301 MAYIMLCRKTSQOEHYVEAR 321
Db 301 MAYIMLCRKTSQOEHYVEAR 321

RESULT 4
Q80WA3 PRELIMINARY; PRT; 280 AA.
AC Q80WA3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein BC025105.
GN Name=BC025105;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farber A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshilynki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skelton U., Smallus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC025105; AAH25105.1;
DR MGD; MGI:2679720; BC025105.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PSS0835; IG_LIKE; 1.
KM Hypothetical protein.
SQ SSOURCE 280 AA; 31467 MW; 3F099AEB96CE8977 CRC64;

Query Match 43.1%; Score 728; DB 2; Length 280;
Best Local Similarity 47.0%; Pred. No. 1.5e-49;
Matches 151; Conservative 29; Mismatches 45; Indels 96; Gaps 2;

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Qy 61 GSDPVTIFLRDSSGDHIIQAKYQGRHLVSHKVPDVSILQSTLEMDRSHYTCVWTQPT 120
Db 61 GSDSVTLFLRDSITGDHIIQAKYGRKLVSHKVPDVSILQSTLEMDRSHYTCVWTQPT 120
Qy 121 DGNQVVDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRSILQCGARSGSPISYIWKQ 180
Db 121 DGNQVVDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRSILQCGARSGSPISYIWKQ 180
Qy 121 DGNQVVDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRSILQCGARSGSPISYIWKQ 180
Db 121 DGNQVVDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRSILQCGARSGSPISYIWKQ 180
Qy 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQGVSEHSDIVKRVVNDSSKLTXTK 240
Db 181 QTNNOEPKXVATLSTLLFKPAVIADSGSYFCTAGQGVSEHSDIVKRVVNDSSKLTXTK 240
Qy 142 -----RIN 144
Db 142 -----RIN 144
Qy 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLIISLCMVFT 300
Db 241 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLIISLCMVFT 300
Qy 145 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLIISLCMVFT 204
Db 145 TEAPTTMTYPLKATSTYKQSWMDTMDGYLGSTAGPGKSLPVFAILLIISLCMVFT 204
Qy 301 MAYIMLCRKTSQOEHYVEAR 321
Db 301 MAYIMLCRKTSQOEHYVEAR 321
Qy 205 IPYILFRCTPFOOEYVYGVSR 225
Db 205 IPYILFRCTPFOOEYVYGVSR 225

RESULT 5
BAC30780 PRELIMINARY; PRT; 280 AA.
AC BAC30780;
DT 14-APR-2004 (Tremblrel. 27, Created)
DT 14-APR-2004 (Tremblrel. 27, Last sequence update)
DT 14-APR-2004 (Tremblrel. 27, Last annotation update)
DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,
DE clone:A53061A1 product:hypothetical immunoglobulin and major
DE histocompatibility complex domain/immunoglobulin subtype containing
DE protein, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

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RA Zhang Z., Henzel W. ;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites." ;
 RL Submitted (JUN-2004) to Swiss-Prot.
 CC -1- FUNCTION: Seems to plays a role in epithelial tight junction
 CC formation. Appears early in primordial forms of cell junctions and
 CC recruits PAR3. The association of the PAR6-PAR3 complex may
 CC prevent the interaction of PAR3 with JAM1, thereby preventing
 CC tight junction assembly (By similarity). Plays a role in
 CC regulating monocyte transmigration involved in integrity of
 CC epithelial barrier. Involved in platelet activation.
 CC -1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
 CC association between PAR3 and PAR6 probably disrupts this
 CC interaction (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Localized at tight junctions of both
 CC epithelial and endothelial cells.
 CC -1- SIMILARITY: Belongs to the immunoglobulin-like V-type domains.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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DR EMBL; AF11713; AAD2050.1; -
 DR EMBL; AF207907; AAR22829.1; -
 DR EMBL; AF172398; AAD48877.1; -
 DR EMBL; AL136649; CAB66584.1; -
 DR EMBL; AY358896; AAG89255.1; -
 DR EMBL; BC001533; AA01533.1; -
 DR PIR; A59406; S56749.
 DR PDB; 1NE0; X-ray; A/B=25-233.
 DR Genew; HGNC:14685; F1LR.
 DR MIM; 605721; -
 DR GO; GO:0005911; C:intracellular junction; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
 FT CHAIN 1 27
 FT DOMAIN 28 299 Junctional adhesion molecule 1.
 FT TRANSMEM 239 259 Extracellular (Potential).
 FT DOMAIN 260 299 Potential.
 FT DOMAIN 28 125 Cytoplasmic (Potential).
 FT DISULFID 135 228 Ig-like V-type 1.
 FT DISULFID 50 109 Ig-like V-type 2.
 FT DISULFID 153 212 Potential.
 FT CARBOHYD 185 185 Potential.
 SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 1; Length 299;
 Best Local Similarity 26.5%; Pred. No. 6.6e-06;
 Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHTVDTYGRPILEVPSVTGPMKGDVNLPTCTYDPLQGYQVLYKMLVOR 60
 DB 17 LAILLGLSLAGSVTVHS-SEPEVRIPEN-----NPKVLSGCAV---SGFSSPRVEM--- 62
 QY 61 GSDPVTIFLRDSSGDHIQAKYQGRRLVSHK-----VPGDVSILSTLEMDRSHYTCYEV 115
 DB 63 -----KPDGDTTRLVLCYNNKKTASJEDRTPLPTGTRFSVTRR--DTGTYTCMV 111
 QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTSGYGFVPGQKRISLQCAR-GSPDIS 174
 DB 112 SEEGGNSYGEVKKVLIYL-----VPSKPTVNIPS-----SATIGNRAVLTCSEDDGSPFSE 163

QY 175 YIYWK-----QQTN-----NOEPIKVAATLSTLLFPKPAVIADSGSYFCTAKQVSGEOR 222
 DB 164 YTFWKGQIVMPTNPKSTRAFSSSYVNLPTTGLVFDPLASDTEGYSCARNGYGTPT 223
 QY 223 SDIVK 227
 DB 224 SNAVR 228

RESULT 7
 AAG28379
 ID AAG28379 PRELIMINARY; PRT; 299 AA.
 AC AAG28379;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE F11 receptor protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20537956; Pubmed=11087121;
 RA Gupta S.K., Pillariseti K., Ohlstein E.H.;
 RT "Platelet agonist F11 receptor is a member of the immunoglobulin
 RT superfamily and identical with junctional adhesion molecule (JAM).
 RT regulation of expression in human endothelial cells and macrophages." ;
 RL IUBMB Life 50:51-56(2000).
 DR EMBL; AF19495; AAG28379.1; -
 DR KW Receptor

SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 2; Length 299;
 Best Local Similarity 26.5%; Pred. No. 6.6e-06;
 Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHTVDTYGRPILEVPSVTGPMKGDVNLPTCTYDPLQGYQVLYKMLVOR 60
 DB 17 LAILLGLSLAGSVTVHS-SEPEVRIPEN-----NPKVLSGCAV---SGFSSPRVEM--- 62
 QY 61 GSDPVTIFLRDSSGDHIQAKYQGRRLVSHK-----VPGDVSILSTLEMDRSHYTCYEV 115
 DB 63 -----KPDGDTTRLVLCYNNKKTASJEDRTPLPTGTRFSVTRR--DTGTYTCMV 111
 QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTSGYGFVPGQKRISLQCAR-GSPDIS 174
 DB 112 SEEGGNSYGEVKKVLIYL-----VPSKPTVNIPS-----SATIGNRAVLTCSEDDGSPFSE 163
 QY 175 YIYWK-----QQTN-----NOEPIKVAATLSTLLFPKPAVIADSGSYFCTAKQVSGEOR 222
 DB 164 YTFWKGQIVMPTNPKSTRAFSSSYVNLPTTGLVFDPLASDTEGYSCARNGYGTPT 223
 QY 223 SDIVK 227
 DB 224 SNAVR 228

RESULT 8
 BAC11436
 ID BAC11436 PRELIMINARY; PRT; 299 AA.
 AC BAC11436;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE cDNA Pl390671 file, clone PLACE1005544, moderately similar to Mus
 DE musclic junctional adhesion molecule (Jam) mRNA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC TISSUE=placenta;
RA Iseogi T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Nakamatsu A., Nakamura Y., Kojima S., Nagai K.,
RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nishimura K.,
RT "NEBO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075152; BAC11436.1; -.
SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 6.6e-06;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHTVDTYGRPILEVPSVTPGPKGVNLPCTYDPLQGYQVLYKMLVQR 60
DB 17 LAILLCSLALGSYTVHS-SEPEVRIPEN-----NPKLSGCAV---SGFSSPREVW---- 62
QY 61 GSDPVITFLRDSGDHIQQAQYQGRILVSHK-----VPGDVSQQLSTLEMDRSHYTCV 115
DB 63 -----KPDGDTTRLVLCYNNKKTASIEDKVTPLPGITRKSVTR--DTGYTCMV 111
QY 116 TWQTPGNOVVRDKITELRVQKLSVKPTVTSYGCVTPGQWRISLQCAR-GSPPI 174
DB 112 SEEGNSYGEVKKVLYL-----VPSKPTVNIPS---SATIGNRAVLTCSEDDGSPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVALTSLLEPRKAVIADSGSFCTAKQVSEQH 222
DB 164 YTMFKGIVMPINPKSTRAFSNSSVYLNPTTGBLVDPDLSASDTGEVSCEARNGYGT 223
QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 9
AA084556 PRELIMINARY; PRT; 299 AA.
ID AA084556;
AC AA084556;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE JAM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wenzel K., Felix S.B., Flachmeier C., Heere P., Schulze W.,
RA Grunewald I., Pankow H., Hewelt A., Scherneck S., Bauer D.,
RA Hoehe M.R.,
RT "Identification and Characterization of KAT, a Novel Gene
RT Preferentially Expressed in Several Human Cancer Cell Lines."
RL Biol. Chem. 384:763-775(2003).
RL EMBL; AF940407; AA084556.1; -.
SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 10.6%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 6.6e-06;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLGLHTVDTYGRPILEVPSVTPGPKGVNLPCTYDPLQGYQVLYKMLVQR 60
DB 17 LAILLCSLALGSYTVHS-SEPEVRIPEN-----NPKLSGCAV---SGFSSPREVW---- 62
QY 61 GSDPVITFLRDSGDHIQQAQYQGRILVSHK-----VPGDVSQQLSTLEMDRSHYTCV 115
DB 63 -----KPDGDTTRLVLCYNNKKTASIEDKVTPLPGITRKSVTR--DTGYTCMV 111
QY 116 TWQTPGNOVVRDKITELRVQKLSVKPTVTSYGCVTPGQWRISLQCAR-GSPPI 174
DB 112 SEEGNSYGEVKKVLYL-----VPSKPTVNIPS---SATIGNRAVLTCSEDDGSPSE 163

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DB 112 SEEGNSYGEVKKVLYL-----VPSKPTVNIPS---SATIGNRAVLTCSEDDGSPSE 163
QY 175 YIMYK-----QQTN-----NOEPIKVALTSLLEPRKAVIADSGSFCTAKQVSEQH 222
DB 164 YTMFKGIVMPINPKSTRAFSNSSVYLNPTTGBLVDPDLSASDTGEVSCEARNGYGT 223
QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 10
A33 HUMAN
ID A33 HUMAN STANDARD; PRT; 319 AA.
AC 099795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN Name=GPA33;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catmel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Rittler G., Cohen L., Welt S., Old L.J., Nice B.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Rittler G., Cohen L.S., Nice B.C., Catmel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium."
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC -1- FUNCTION: May play a role in cell-cell recognition and signaling.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC -1- PTM: N-glycosylated, contains approximately 8 kDa of N-linked
CC carbohydrate.
CC -1- PTM: Palmitoylated.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U79725; AAC0957.1; -.
DR HSSP; O88792; 1F97.
DR Genew; HGNC:4445; GPA33.
DR MIM; 602171; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Antigen; Direct protein sequencing; Glycoprotein;

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RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069723; AAH69745.1; -.
 KM Transmembrane.
 SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAR45C2408E CRC64;

Query Match 10.5%; Score 177; DB 2; Length 319;
 Best Local Similarity 27.5%; Pred. No. 9,4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

QY 4 LGLLLGLHLYDTYGRPLLEVPESVTPGPKG-DVNLPCITYDPLQGYTVLVKM--LVQR 60
 DB 8 VMLTLCARVTVDAIS--VETPODVLRASQGSVTLPTCTHTSTSSRGLIQMDKLLLT 64
 QY 61 GSDPVITFLRDSGDHIQQAQYQGRLVSHKV-PGCVSLQSLTLEMDRSHYTCVYWTQ 119
 DB 65 HTRRVYIV-PFSKNVYIHGLYKKNRVSISNNAEQSDASITIIDQLTMADNGTCEVSIMS 123
 QY 120 P-DGNOVVDKITELRVQKLSVSKPTVTGSGYGFVTPQGMISLQCGAR-GSPPISYIV 177
 DB 124 DLKGN-----TKSRVRLVLVPPSKPCGIEGERT-IGNNIQLTCQSGESPTPQYSW 175
 QY 178 YKQQTNNQ-----PIKVAITSLTLFPAVIAADSGSYFCTAKGVGSE 220
 DB 176 KRYNIINQEQPLAQPASGQPVSLKNIST-----DTSGYITCTSSNEBGTQ 220

RESULT 13

AAH69745 PRELIMINARY; PRT; 319 AA.

AC AAH69745; 1
 DT 20-MAY-2004 (TrEMBLrel. 27, Created)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Transmembrane glycoprotein A33.,

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NC NCBI_TaxId=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalov D.E., Schmeich A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069745; AAH69745.1; -.
 KM Transmembrane.
 SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAR45C2408E CRC64;

Query Match 10.5%; Score 177; DB 2; Length 319;

Best Local Similarity 27.5%; Pred. No. 9,4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

QY 4 LGLLLGLHLYDTYGRPLLEVPESVTPGPKG-DVNLPCITYDPLQGYTVLVKM--LVQR 60
 DB 8 VMLTLCARVTVDAIS--VETPODVLRASQGSVTLPTCTHTSTSSRGLIQMDKLLLT 64
 QY 61 GSDPVITFLRDSGDHIQQAQYQGRLVSHKV-PGCVSLQSLTLEMDRSHYTCVYWTQ 119
 DB 65 HTRRVYIV-PFSKNVYIHGLYKKNRVSISNNAEQSDASITIIDQLTMADNGTCEVSIMS 123
 QY 120 P-DGNOVVDKITELRVQKLSVSKPTVTGSGYGFVTPQGMISLQCGAR-GSPPISYIV 177
 DB 124 DLKGN-----TKSRVRLVLVPPSKPCGIEGERT-IGNNIQLTCQSGESPTPQYSW 175
 QY 178 YKQQTNNQ-----PIKVAITSLTLFPAVIAADSGSYFCTAKGVGSE 220
 DB 176 KRYNIINQEQPLAQPASGQPVSLKNIST-----DTSGYITCTSSNEBGTQ 220

RESULT 14

AAH69761 PRELIMINARY; PRT; 319 AA.

AC AAH69761; 1
 DT 20-MAY-2004 (TrEMBLrel. 27, Created)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Transmembrane glycoprotein A33.,

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NC NCBI_TaxId=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalov D.E., Schmeich A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069761; AAH69761.1; -.
 KM Transmembrane.
 SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAR45C2408E CRC64;

Query Match 10.5%; Score 177; DB 2; Length 319;
 Best Local Similarity 27.5%; Pred. No. 9,4e-06;
 Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

QY 4 LGLLLGLHLYDTYGRPLLEVPESVTPGPKG-DVNLPCITYDPLQGYTVLVKM--LVQR 60
 DB 8 VMLTLCARVTVDAIS--VETPODVLRASQGSVTLPTCTHTSTSSRGLIQMDKLLLT 64


```

Qy 61 GSPPTVIFLRDSSGHDHIOQAQKQGRHVSHKV-PEGVSLQJLSTLEMDRSHYTCQEMQJ 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 HTRRVAIW-PFSKNKIYHIGELYNKRYSJNNAGSDASITTDQLTMANQTECVSLMS 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 120 P-IGNQNVVDKLTETELFVQKLSVSKPTVTGSGYGFVEQGRMRISQCCAR-GSPPIXYW 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 DLEGN-----TKSRVRLIVLPSPKPCGIEGETI-IGNNIQLTCSKSGSPPTQYSW 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 178 YKOQTNQJ-----PIKATVSTLEFPRAVIADSGSYFTAKQVSE 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 KRNIINQDEPLAQPASGQPVSLKSIIST-----DHSGYITCTISNBEQTQ 220

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Db      124 DLEGN-----TKSNRLVLVPPSKKECGIEGTI-IGNNIQLTQSKSGSPTPYSW 175
OY      178 YKQQTNOE-----PIVATLSTLLFKPAVIADSGSYFTAKQVSE 220
Db      176 KRYNIINOEPPLAQPASGPVSLKRIST-----DTSGYICTSSNEBCTQ 220

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Search completed: January 4, 2005, 06:10:20
Job time : 175 secs

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Job time : 175 secs

RESULT	15
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ID	AAH69789;
AC	20-MAY-2004 (TREMBlrel. 27, Created)
DT	20-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT	20-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE	Transmembrane glycoprotein A33, .
GN	GPA33.
OS	Homo sapiens (Human) .
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=PCR rescued clones;
RX	MEDLINE=22388257; PubMed=1477932.
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Stauberg R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA	Aleschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Zeehan H., Moore T., Max S.I., Wang J., Heish F.,
RA	Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Steptelon M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein W.J., Udaft T.B., Toshiyuki S., Carrinci P., Prange C.,
RA	Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA	Villalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettelman M., Madden A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakeley R.W., Touchman V.W., Green E.D., Dickson M.C.,
RA	Rodriguez R.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
RA	Krzywnicki M.I., Skalski U., Smallus D.B., Scherch A., Schein J.R.,
RA	Jones S.J., Marx M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=PCR rescued clones;
RA	Strauberg R.;
RL	Submitted (APR-2004) to the EMBL/genbank/DBJ databases.
DR	EMBL; BC0659789; AAH69789.1; ..
KM	Transmembrane
SC	SEQUENCE 319 AA; 35632 MW; 9BEC7AFAF5C2408E ² CRC64;
Query Match	10.5%; Score 177; DB 2; Length 319;
Best Local Similarity	27.5%; Pred. No. 9.4e-06;
Matches	64; Conservative 39; Mismatches 94; Indels 36; Gaps 11.
QY	4 ILGLILLHLVYDYGRILEVPSVATGPMKG-DYNLECTPDLOGITVLVKW-LYQR 60
DB	8 VLMTICAVRVTVDAIS---VETPQOVLASQGSKSTLPCTHTSTSSREGILQWKLLT 64
QY	61 GSDPTTIRLRSSGDHIQQAQYGRALSHKV-PGDVSLQLSTLEMDSRYTCVWT 119
DB	65 HTERLVIV-PEPNKKYIHGELYKORVSI-SNNNAEGSADISTIDQLMAONGTECVSLMS 123
OY	120 P-DGNQVRDKITELRVOKLSVSKRTVTGGSGYGTTFPOGMKRLISLQQCAR-GSPISIV 177

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 06:06:41 ; Search time 27 Seconds
(without alignments)
1143.910 Million cell updates/sec

Title: US-10-767-374-2
Perfect score: 1688
Sequence: 1 MGILLGLLLIGHTVDYTRG.....AYIMLCRKTSQGRHYVEAAR 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178.5	10.6	229	2	S56749
2	172	10.2	7962	2	I38346
3	169	10.0	365	2	UC7780
4	143.5	8.5	1052	2	B49120
5	139.5	8.3	3707	2	S18252
6	138.5	8.2	1323	2	PN0568
7	138.5	8.2	4162	2	T08678
8	136	8.1	584	2	T08678
9	133.5	7.9	5175	2	T20392
10	133.5	7.9	5198	2	T43290
11	133	7.8	1106	1	PFHUGB
12	132.5	7.8	765	2	C42632
13	132.5	7.8	812	2	B42632
14	132.5	7.8	932	2	A42632
15	132.5	7.8	1272	2	S26180
16	132	7.8	1896	2	T08851
17	131	7.8	4391	2	A38096
18	129.5	7.7	1040	2	A34685
19	129.5	7.7	3375	2	T11981
20	129	7.6	1427	2	I51669
21	128.5	7.6	338	2	JC5519
22	127.5	7.6	1906	1	S68235
23	125.5	7.4	1259	2	A43425
24	125	7.4	351	2	JH0396
25	124	7.3	853	1	IJB0NC
26	124	7.3	1344	2	T14316
27	123.5	7.3	458	1	MMMSR1
28	123.5	7.3	521	2	JC1508
29	123.5	7.3	1091	1	IJCNTL

30	122.5	7.3	761	1	IJTHNG
31	122.5	7.3	1258	1	A39540
32	120.5	7.1	458	2	UC1509
33	120.5	7.1	538	2	JC2457
34	120	7.1	1033	2	S19247
35	119.5	7.1	1036	2	S22383
36	119.5	7.1	417	2	JH0394
37	119.5	7.1	464	2	C30127
38	119.5	7.1	463	2	T17346
39	119.5	7.1	526	1	A32164
40	119.5	7.1	725	1	IJMSNG
41	119.5	7.1	725	1	JEO100
42	119.5	7.1	1115	1	IJMSNL
43	119	7.0	467	1	HLMSP3
44	119	7.0	1091	2	A58532
45	119	7.0	26926	1	I38344
46	118.5	7.0	333	2	A31923
47	118.5	7.0	458	2	S68177
48	118.5	7.0	458	2	S23969
49	118.5	7.0	539	2	A44783
50	118.5	7.0	816	2	A49151
51	118.5	7.0	1011	2	T13669
52	118.5	7.0	1694	2	S50065
53	118	7.0	547	1	S28904
54	118	7.0	1338	2	S09982
55	117.5	7.0	338	2	UC4776
56	117.5	7.0	344	2	A27681
57	117.5	7.0	1092	1	JN0635
58	117.5	7.0	1239	1	A32579
59	117	6.9	739	2	J50675
60	117	6.9	858	1	IJRNMC
61	117	6.9	1447	2	A54100
62	116.5	6.9	806	2	A35963
63	116.5	6.9	1040	2	A49356
64	116.5	6.9	1051	2	A39712
65	116	6.9	344	2	I56551
66	116	6.9	6658	2	T13931
67	115.5	6.8	222	2	S03421
68	115.5	6.8	223	2	A40131
69	115.5	6.8	309	2	I49522
70	115.5	6.8	725	2	JEO099
71	115.5	6.8	738	2	A40096
72	115.5	6.8	1257	1	A41060
73	115	6.8	1209	2	T42718
74	114.5	6.8	478	2	I53960
75	114.5	6.8	521	2	S34338
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78	114.5	6.8	1173	2	T25893
79	114	6.8	544	2	UC5018
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81	113	6.7	1277	2	T30532
82	112.5	6.7	321	2	JH0395
83	112.5	6.7	345	2	UC4025
84	112.5	6.7	1259	2	S36126
85	112.5	6.7	2029	1	TDFRLK
86	112	6.6	946	1	A47299
87	112	6.6	976	2	T29583
88	112	6.6	1273	2	T42405
89	111	6.6	806	1	TVHUP3
90	111	6.6	6642	2	T29757
91	110.5	6.5	349	2	A34815
92	110.5	6.5	518	2	UC4024
93	110	6.5	499	2	S33766
94	110	6.5	917	2	I48950
95	110	6.5	1070	2	JC4593
96	110	6.5	1880	2	T18531
97	110	6.5	2295	2	C68369
98	109.5	6.5	338	2	UC1238
99	109.5	6.5	345	2	UC1239
100	109.5	6.5	526	2	S70587
101	109.5	6.5	1336	2	I60598
102	109	6.5	547	2	B45808

neural cell adhesion
neural cell adhesion
biliary glycoprotein
vascular cell adhesion
cell adhesion protein
axonal precursor
biliary glycoprotein
transmembrane protein
hypothetical protein
biliary glycoprotein
neural cell adhesion
neural cell adhesion
poliovirus receptor
glial cell membrane
titin, cardiac muscle
amalgam protein
C-CAM2a protein
cell adhesion molecule
ecto-ATPase precursor
fibroblast growth
neurotactin - fr
sialoadhesin - fr
neurotactin - fr
intercellular adhesion
protein-tyrosine kinase
limbic system-associated
non-specific cross-
neural cell adhesion
neuroglial cell adhesion
vascular cell adhesion
neural cell adhesion
tumor suppressor protein
protein-tyrosine kinase
transient axonal
kinase-like protein
neurotactin - rat
protectin - fruit
T-cell receptor de
T-cell receptor de
gene B7-2 protein
neural cell adhesion
platelet endothelial
neural cell adhesion
probable neural cell
PRR2 alpha - human
biliary glycoprotein
PRR2 delta - human
neural cell adhesion
hypothetical protein
intercellular adhesion
poliovirus receptor
neural cell adhesion
biliary glycoprotein
opioid-binding protein
neural cell adhesion
protein-tyrosine kinase
ractor-related receptor
hypothetical protein
sax-3 protein - Ca
fibroblast growth
protein UNC-89 - C
carcinoembryonic antigen
poliovirus receptor
platelet-derived growth
telencephalin precursor
protein-tyrosine kinase
tracrin - medicine
protein unc-52 (lim
opioid-binding protein
opioid-binding protein
butyrylcholinesterase
F1t-1 tyrosine kinase
B-lymphocyte antigen

103	109	6.5	646	2	I38049	cell surface glyco
104	108.5	6.4	345	2	S03199	opoid-binding pro
105	108.5	6.4	416	2	A54017	colon carcinoma-as
106	108.5	6.4	1328	2	T23007	hypothetical prote
107	108	6.4	526	2	A37821	butyrophilin - bov
108	107	6.3	773	1	QRRBG	secretory componen
109	106.5	6.3	354	1	S42938	proteoglycan link
110	106.5	6.3	1227	2	T23004	hypothetical prote
111	106.5	6.3	1232	2	T43027	neural cell adhesi
112	106	6.3	919	2	T32541	unc-5 protein - Ca
113	106	6.3	947	2	B44294	unc-5 protein, lon
114	106	6.3	1040	2	A57638	receptor tyrosine
115	106	6.3	1098	1	PFMGRB	platelet-derived g
116	106	6.3	1103	2	T22889	hypothetical prote
117	105.5	6.2	423	2	T29549	hypothetical prote
118	105.5	6.2	582	1	BNRT3S	myelin-associated
119	105.5	6.2	626	1	BNRT3	myelin-binding gr
120	105.5	6.2	662	2	C40862	heparin-binding gr
121	105.5	6.2	729	2	A56795	fibroblast growth
122	105.5	6.2	733	2	T49293	fibroblast growth
123	105.5	6.2	822	1	TVHURG	fibroblast growth
124	105.5	6.2	822	2	I49289	fibroblast growth
125	105.5	6.2	822	2	S29840	fibroblast growth
126	105.5	6.2	940	2	A40985	prolactin - fruit
127	104.5	6.2	268	2	T23555	hypothetical prote
128	104.5	6.2	392	2	B44194	poliovirus recepto
129	104.5	6.2	417	2	A44194	poliovirus recepto
130	104.5	6.2	1184	2	T09484	cartilage intermed
131	104.5	6.2	2222	2	TL3524	sdh protein - frul
132	104	6.2	299	1	AHRB	ig alpha chain C r
133	104	6.2	338	2	S09276	heparin-binding gr
134	104	6.2	801	2	A48991	fibroblast growth
135	104	6.2	802	2	I55363	receptor tyrosine
136	104	6.2	828	2	I38912	luteal blood gro
137	103.5	6.1	628	2	I38000	fibroblast growth
138	103.5	6.1	819	1	TVCHFG	fibroblast growth
139	103.5	6.1	822	1	TVMSFG	fibroblast growth
140	103.5	6.1	824	2	S36439	fibroblast growth
141	103.5	6.1	832	2	JH0393	fibroblast growth
142	103.5	6.1	1356	2	TJ1402	protein-tyrosine k
143	103.5	6.1	1612	2	T30805	duct protein - mo
144	103	6.1	811	2	A41054	fasciclin II, tran
145	103	6.1	873	2	B41054	fasciclin II p1-11
146	103	6.1	2783	2	T34416	hypothetical prote
147	102.5	6.1	318	2	P72171	K9R protein - vari
148	102.5	6.1	1176	2	JN0583	myosin-light-chain
149	102.5	6.1	1651	2	TL1460	transmembrane rece
150	102	6.0	637	2	B33785	myelin-associated
151	102	6.0	702	2	A36319	carcinoembryonic a
152	102	6.0	800	1	TVHURF	protein-tyrosine k
153	102	6.0	871	1	I48696	protein-tyrosine k
154	102	6.0	881	1	I48697	protein-tyrosine k
155	101.5	6.0	392	1	RMHURD	hemolitus recepto
156	101.5	6.0	413	2	S65948	hemolitus recepto
157	101.5	6.0	413	2	A37778	hemolitus recepto
158	101.5	6.0	417	1	RMHUPA	poliovirus recepto
159	101.5	6.0	599	2	TL6774	hypothetical prote
160	101.5	6.0	898	2	A40114	fasciclin II precu
161	101.5	6.0	1260	1	S05479	neural cell adhesi
162	101	6.0	267	2	A38442	probable tumor sup
163	101	6.0	584	2	I50419	s-glycerin precuro
164	101	6.0	620	2	JH0593	Schwann cell myel
165	101	6.0	797	2	S38579	fibroblast growth
166	101	6.0	868	2	A46512	CD22 homolog/B lym
167	101	6.0	890	1	A53743	protein-tyrosine k
168	101	6.0	1742	2	S24600	prolactin - fruit
169	101	6.0	6831	2	A88852	protein unc-22 [lm
170	101	6.0	6839	2	S57242	twichin [leimlari
171	101	6.0	7160	2	T27935	hypothetical prote
172	100.5	6.0	355	1	LKCH	proteoglycan link
173	100.5	6.0	408	1	LKRT2	proteoglycan link
174	100.5	6.0	647	2	A35648	B-cell adhesion pr
175	100.5	6.0	700	1	HYHUMB	meprin A [EC 3.4.2
176	100.5	6.0	802	1	TVHUP4	fibroblast growth
177	100.5	6.0	847	2	JH0371	B-cell adhesion pr
178	100	5.9	354	1	LKRU	proteoglycan link
179	100	5.9	520	1	S44099	brain-derived neur
180	100	5.9	818	1	S44098	brain-derived neur
181	100	5.9	1021	2	I39207	leukocyte surface
182	99.5	5.9	459	2	A46254	CD4 precursor - ra
183	99.5	5.9	626	1	A61084	myelin-associated
184	99.5	5.9	790	2	A39627	protein-tyrosine k
185	99.5	5.9	1028	2	I58164	BiG-1 protein - ra
186	99.5	5.9	1379	2	UC4954	vascular endotheli
187	99.5	5.9	1666	2	A48594	skeletal - mouse
188	99	5.9	275	2	H35216	FP31 protein - fow
189	99	5.9	313	2	J01862	31R protein - vari
190	99	5.9	424	2	B35109	pregnancy-specific
191	99	5.9	458	1	RMHUT4	T-cell surface gly
192	99	5.9	773	2	T46283	hypothetical prote
193	99	5.9	812	1	A36477	fibroblast growth
194	99	5.9	818	2	UC4058	fibroblast growth
195	99	5.9	862	2	I49583	fibroblast growth
196	99	5.9	1375	2	T13822	differentiation an
197	99	5.9	1526	2	T13823	fraxzed gene prot
198	98.5	5.8	288	2	T24824	hypothetical prote
199	98.5	5.8	602	2	A45769	acetylcholine rece
200	98.5	5.8	1021	2	T42634	connectin/citin -
201	98.5	5.8	1330	2	S49010	embryonic receptor
202	98.5	5.8	1333	2	T78875	receptor tyrosine
203	98	5.8	880	1	UC4166	protein-tyrosine k
204	98	5.8	880	2	B53743	protein-tyrosine k
205	98	5.8	1499	2	I50212	protein-tyrosine-p
206	97.5	5.8	144	2	S36308	T-cell receptor de
207	97.5	5.8	354	1	S04243	proteoglycan link
208	97.5	5.8	476	1	A35104	brain-derived neur
209	97.5	5.8	588	2	I37202	B-CM protein - hu
210	97.5	5.8	729	2	A45120	fibroblast growth
211	97.5	5.8	764	2	A49448	irregular chiasm C
212	97.5	5.8	821	1	S06943	brain-derived neur
213	97.5	5.8	876	2	I49152	protein-tyrosine k
214	97.5	5.8	1348	2	AH1115	cell surface prote
215	97.5	5.8	1443	2	I50600	neogenin - chicken
216	97	5.7	116	2	D24891	T-cell receptor al
217	97	5.7	307	2	S55596	hypothetical prote
218	97	5.7	474	1	OMHUIB	alpha-1-B-glycopro
219	97	5.7	739	2	A41288	vascular cell adhe
220	97	5.7	751	2	T42597	DNA helicase/prima
221	97	5.7	824	2	S24108	protein-tyrosine k
222	97	5.7	1028	2	A53449	plasmacytoma-assoc
223	97	5.7	1147	2	A59307	myosin-light-chain
224	97	5.7	1274	2	S55050	cardiac myosin-bin
225	97	5.7	1367	2	A41228	protein-tyrosine k
226	97	5.7	1535	2	S46224	peroxidasin - frui
227	96.5	5.7	288	2	A31326	T-cell receptor de
228	96.5	5.7	313	2	T28598	hypothetical prote
229	96.5	5.7	772	2	T13078	KIAA0992 protein -
230	96.5	5.7	1200	2	TL1404	hyalain - sea urchi
231	96.5	5.7	2013	2	AD1129	probable peptidogl
232	96	5.7	243	2	S25755	Ig lambda chain -
233	96	5.7	407	2	C82428	glucose-1-phosphat
234	96	5.7	462	2	I38404	neu differentiatio
235	96	5.7	640	2	A43273	heretugulin precuro
236	96	5.7	739	2	JN0581	vascular cell adhe
237	96	5.7	1262	1	B48758	protein-tyrosine-p
238	96	5.7	1496	1	A48758	protein-tyrosine-p
239	96	5.7	1530	2	AH1396	peptidoglycan anch
240	96	5.7	6805	2	S20901	ctitin - rabdt (fr
241	95.5	5.7	243	2	A53244	leukocyte antigen
242	95.5	5.7	1132	2	A35089	myosin-binding pro
243	95	5.6	137	2	I46628	rearranged T-cell
244	95	5.6	814	1	A39752	fibroblast growth
245	95	5.6	994	2	I49276	c-mer tyrosine kin
246	95	5.6	1450	2	A44027	165k myofibrillar
247	95	5.6	1501	2	I58148	protein-tyrosine-p
248	95	5.6	1863	2	S46217	protein-tyrosine-p

249	95	5.6	1907	2	S50893	protein-tyrosine-p
250	95	5.6	1945	2	T13937	plexin A - fruit f
251	94.5	5.6	135	2	S36314	T-cell receptor de
252	94.5	5.6	315	1	HNW24X	hemagglutinin prec
253	94.5	5.6	328	2	S30444	Sr2 protein - huma
254	94.5	5.6	477	1	I73631	brain-derived neur
255	94.5	5.6	588	2	JH0506	adhesion molecule
256	94.5	5.6	588	2	A45254	surface glycoprote
257	94.5	5.6	822	1	A56853	brain-derived neur
258	94.5	5.6	875	2	T33434	hypothetical prote
259	94.5	5.6	888	2	S23065	uto protein - mous
260	94.5	5.6	999	2	I38547	novel cellular pro
261	94.5	5.6	1256	2	T03096	CNO protein - rat
262	94	5.6	118	2	I71934	MHC class II T-A-a
263	94	5.6	268	2	A56446	Ig heavy chain V r
264	94	5.6	313	2	H36854	hemagglutinin - va
265	94	5.6	422	2	S32357	glial growth facto
266	94	5.6	583	2	G84829	probable PTR2 fami
267	94	5.6	887	2	AD2009	hypothetical prote
268	94	5.6	943	2	F69543	ATP-dependent RNA
269	94	5.6	1091	2	S01938	contactin precursor
270	94	5.6	1325	2	A64905	ylek protein - Esc
271	93.5	5.5	142	2	S36307	T-cell receptor de
272	93.5	5.5	259	2	JC7109	Sr2V protein - hum
273	93.5	5.5	329	1	A48754	B7-2 antigen - hum
274	93.5	5.5	587	2	JH0454	DW-GRASP precursor
275	93.5	5.5	799	2	S18209	fibroblast growth
276	93	5.5	432	1	RWC274	T-cell surface gly
277	93	5.5	435	2	D33258	neural adhesion pr
278	93	5.5	1018	2	JC4211	versican precursor
279	93	5.5	1643	2	T14274	versican precursor
280	93	5.5	3391	2	T42389	T-cell receptor de
281	92.5	5.5	144	2	S36322	CS86 spliced varia
282	92.5	5.5	275	2	JC7604	pregnancy-specific
283	92.5	5.5	424	2	A34595	fibroblast growth
284	92.5	5.5	713	2	I50128	secretory componen
285	92.5	5.5	764	1	ORHUGS	hypothetical prote
286	92.5	5.5	1321	2	T00382	T-cell receptor al
287	92	5.5	116	2	E24891	Ig light chain V r
288	92	5.5	132	2	A55410	tumor surface anti
289	92	5.5	323	2	A48997	alcam - human
290	92	5.5	583	2	I39428	neu differentiation
291	92	5.5	639	2	I61719	fibroblast growth
292	92	5.5	829	2	JC4583	Ig heavy chain - C
293	92	5.5	1005	2	T18537	hypothetical prote
294	92	5.5	13055	2	T16580	antigen BCM1 precu
295	91.5	5.4	240	2	JL0143	teratocarcinoma gl
296	91.5	5.4	330	2	A29915	interleukin-1 rece
297	91.5	5.4	576	2	A32604	vascular cell adhe
298	91.5	5.4	647	2	B41288	nephrin - human
299	91.5	5.4	1241	2	T37150	probable peptidogl
300	91.5	5.4	2013	2	A11489	hypothetical prote
301	91	5.4	282	2	T17219	cell surface glyco
302	90.5	5.4	309	2	S15674	probable ABC trans
303	90.5	5.4	341	2	B95403	fibroblast growth
304	90.5	5.4	361	2	PN0020	brain-derived neur
305	90.5	5.4	474	1	C39667	brain-derived neur
306	90.5	5.4	476	1	B39667	butyrophilin - mou
307	90.5	5.4	487	2	S65133	cell fusion glycop
308	90.5	5.4	631	1	A48346	brain-derived neur
309	90.5	5.4	631	1	VGNZBD	brain-derived neur
310	90.5	5.4	821	1	A39667	ERBB kinase activa
311	90.5	5.4	860	2	JC5702	ERBB kinase activa
312	90.5	5.4	868	2	UC5701	Ig heavy chain pre
313	90	5.3	380	2	S12839	hypothetical prote
314	90	5.3	526	2	T27581	hypothetical prote
315	90	5.3	789	2	T28714	fibroblast growth
316	90	5.3	821	1	TVHUY2	contactin 1 precu
317	90	5.3	1018	2	A54744	COO protein - huma
318	90	5.3	1240	2	T03097	hypothetical prote
319	90	5.3	1343	2	B90893	hypothetical prote
320	90	5.3	1343	2	D85724	hypothetical prote
321	90	5.3	1355	2	T28715	hypothetical prote
322	89.5	5.3	142	2	S04664	T-cell receptor de
323	89.5	5.3	157	2	S04915	calcium vector pro
324	89.5	5.3	243	2	A37982	pregnancy-specific
325	89.5	5.3	275	2	A28928	titin - mouse (fra
326	89.5	5.3	531	2	S20900	protein-tyrosine k
327	89.5	5.3	823	2	B35963	cadherin 3 precu
328	89.5	5.3	829	1	IJHICP	165k protein, skel
329	89.5	5.3	1465	2	S43529	probably celluloso
330	89.5	5.3	1465	2	C97012	proteoglycan link
331	89	5.3	101	2	A29165	rearranged T-cell
332	89	5.3	145	2	A29165	T-cell receptor de
333	89	5.3	279	2	S04693	pregnancy-specific
334	89	5.3	282	2	C28928	colicin V secretio
335	89	5.3	413	1	IKKCSA	neurotin - goldfis
336	89	5.3	523	2	I50478	heparin-binding gr
337	89	5.3	682	2	A35969	fibroblast growth
338	89	5.3	769	2	S16236	fibroblast growth
339	89	5.3	822	2	A45081	keratinocyte growt
340	89	5.3	822	2	A41794	neutroal cell surf
341	89	5.3	1020	2	S05944	ketlin - fruit fly
342	88.5	5.2	524	2	S33341	chondroitin sulfat
343	88.5	5.2	3562	2	A47171	hypothetical prote
344	88	5.2	131	2	T20334	myelin/oligodendro
345	88	5.2	247	2	A55717	activated B-cell p
346	88	5.2	568	2	A45804	herregulin precursor
347	88	5.2	850	2	JC5700	alcohol dehydrogen
348	88	5.2	1021	2	A57112	polymetric immunog
349	88	5.2	1711	2	AB1283	neural cell adhesi
350	88	5.2	2051	2	T30938	leukocyte antigen-
351	87.5	5.2	205	2	A48929	T-cell receptor de
352	87.5	5.2	246	2	A47712	myeloid cell surfa
353	87.5	5.2	637	2	C43273	HLA-B*33.1, HLA-Aw
354	87.5	5.2	742	2	US0326	hypothetical prote
355	87.5	5.2	757	2	I45956	sagp protein - Cam
356	87.5	5.2	1197	2	T30581	190k protein - hum
357	87.5	5.2	1897	1	TDHUKC	T-cell receptor al
358	87	5.2	139	2	S33032	myeloid cell surfa
359	87	5.2	364	2	A30521	HLA-B*33.1, HLA-Aw
360	87	5.2	365	2	I72171	hypothetical prote
361	87	5.2	818	2	T19120	sagp protein - Cam
362	87	5.2	936	2	I40711	190k protein - hum
363	87	5.2	1451	2	S42167	T-cell receptor al
364	86.5	5.1	110	1	C24891	hemagglutinin prec
365	86.5	5.1	310	1	HNWZRA	class I histocompa
366	86.5	5.1	363	2	JH0542	Mut/Tnux family
367	86.5	5.1	465	2	A82211	protein-tyrosine k
368	86.5	5.1	894	1	A41527	vascular endotheli
369	86.5	5.1	1348	2	S51656	protein-tyrosine k
370	86.5	5.1	1363	2	I58375	hypothetical prote
371	86.5	5.1	1637	2	T46438	protein-tyrosine-p
372	86.5	5.1	1894	2	C54689	hypothetical prote
373	86.5	5.1	2025	2	T21588	probable PPE prote
374	86.5	5.1	3157	2	B70969	T-cell receptor al
375	86	5.1	116	2	B24891	rearranged T-cell
376	86	5.1	150	2	I46624	re-gamma receptor
377	86	5.1	270	2	A34636	Ig alpha chain C r
378	86	5.1	357	2	S09265	interleukin-1 rece
379	86	5.1	328	2	S17428	hypothetical prote
380	86	5.1	421	2	T46266	fibroblast growth
381	86	5.1	480	2	B56182	pyruvate kinase (E
382	86	5.1	497	2	JC2456	hypothetical prote
383	86	5.1	964	2	T15746	protein-tyrosine k
384	86	5.1	975	1	TVMSKT	immunoglobulin-lik
385	86	5.1	1327	2	T09402	hypothetical prote
386	86	5.1	1345	2	H90975	probable invasin (
387	86	5.1	1417	2	H90670	probable invasin e
388	86	5.1	1417	2	D85521	probable invasin Z
389	86	5.1	2650	2	E85822	Ig kappa chain V r
390	85.5	5.1	210	2	A56169	Ig kappa chain V r
391	85.5	5.1	216	2	J80245	Ig lambda chain V r
392	85.5	5.1	218	2	S68241	Ig kappa chain V r
393	85.5	5.1	302	2	C36464	fibroblast growth
394	85.5	5.1	329	2	A44065	fibroblast growth

395	85.5	5.1	330	2	I46691	CD86 precursor - r
396	85.5	5.1	332	2	C83610	lactate-binding pr
397	85.5	5.1	338	2	B48899	beta-lactamase (EC
398	85.5	5.1	397	2	C43354	pregnancy-specific
399	85.5	5.1	419	2	JC4123	pregnancy-specific
400	85.5	5.1	677	2	S14683	Ig mu chain precur
401	85.5	5.1	636	2	I61718	neu differentiatio
402	85.5	5.1	869	2	A86983	conserved hypochet
403	85.5	5.1	869	2	S72760	ppe1 protein - Myc
404	85.5	5.1	1094	2	S22573	DNA-directed DNA p
405	85.5	5.1	1518	2	S37928	probable purine nu
406	85.5	5.1	1691	1	D54689	protein-tyrosine-p
407	85.5	5.1	2541	2	T29340	hypothetical prote
408	85	5.0	104	2	S07705	T-cell receptor al
409	85	5.0	137	2	S36303	T-cell receptor de
410	85	5.0	166	2	A33402	pregnancy-specific
411	85	5.0	247	2	S58394	myelin/oligodendro
412	85	5.0	265	2	A55811	carcinoembryonic a
413	85	5.0	273	2	B28928	pregnancy-specific
414	85	5.0	428	2	I57486	pregnancy-specific
415	85	5.0	428	2	J50032	pregnancy-specific
416	85	5.0	480	2	A56182	fibroblast growth
417	85	5.0	466	2	P00666	envelope protein -
418	85	5.0	769	1	QKRTGS	secretory componen
419	85	5.0	776	2	S41628	genome polypeptide
420	85	5.0	904	2	I38757	homolog of Drosoph
421	85	5.0	913	1	A47543	R-cadherin precurs
422	85	5.0	926	2	I38756	homolog of Drosoph
423	85	5.0	1005	2	A42265	alpha-mannosidase
424	85	5.0	2325	2	A61208	chondroitin sulfat
425	85	5.0	2409	1	A60979	versican precursor
426	84.5	5.0	241	2	S32359	glial growth facto
427	84.5	5.0	266	2	T29613	hypothetical prote
428	84.5	5.0	286	2	A28833	carcinoembryonic a
429	84.5	5.0	419	2	A33258	pregnancy-specific
430	84.5	5.0	419	2	A31135	pregnancy-specific
431	84.5	5.0	432	2	S30193	T-cell surface gly
432	84.5	5.0	436	2	B69371	bile acid-inducibl
433	84.5	5.0	457	2	A27449	T-cell surface gly
434	84.5	5.0	474	2	S15590	Ig heavy chain - h
435	84.5	5.0	568	2	I58106	gene DM-N9 protei
436	84.5	5.0	642	2	E72215	oligopeptide ABC t
437	84.5	5.0	795	2	T21487	hypothetical prote
438	84.5	5.0	821	1	TVMSBK	fibroblast growth
439	84.5	5.0	941	1	TVMTMD	protein-tyrosine k
440	84.5	5.0	980	1	TVCTMD	macrophage colony-
441	84.5	5.0	1142	2	S36845	myosin-binding pro
442	84.5	5.0	1349	2	A11476	cell surface prote
443	84.5	5.0	1433	2	T30261	chitinase (EC 3.2.
444	84.5	5.0	2508	2	S61441	surface-associated
445	84	5.0	238	2	C90909	probable major tai
446	84	5.0	255	2	JC7593	SH2 domain-contain
447	84	5.0	315	1	HNWZVT	hemagglutinin prec
448	84	5.0	315	2	T37438	hemagglutinin - va
449	84	5.0	321	2	D39371	Ig V-region-like B
450	84	5.0	406	2	E43354	Ig V-region-specific
451	84	5.0	452	1	MHHU	Ig mu chain C regi
452	84	5.0	453	2	S37768	Ig mu chain C regi
453	84	5.0	473	1	MHHUM	Ig mu chain C regi
454	84	5.0	621	2	B57431	myosin-binding C-P
455	84	5.0	781	2	S51592	Xyln precursor - R
456	84	5.0	939	2	AF2503	hypothetical prote
457	84	5.0	1065	2	H95321	NoIG efflux transp
458	84	5.0	1912	2	A56178	protein-tyrosine-p
459	84	5.0	2397	1	A55535	versican precursor
460	83.5	4.9	264	2	F27579	T-cell receptor al
461	83.5	4.9	275	1	RWHUAC	T-cell receptor al
462	83.5	4.9	288	1	A45803	B-cell-restricted
463	83.5	4.9	317	2	JL0118	Fc gamma (IgG) rec
464	83.5	4.9	339	2	AG0010	exported sulfate-b
465	83.5	4.9	344	1	S09264	Ig alpha chain C r
466	83.5	4.9	344	1	RWRTC2	T-cell surface gly
467	83.5	4.9	363	2	S07113	class I histocompa
468	83.5	4.9	372	2	C39371	Ig V-region-like B
469	83.5	4.9	496	2	S60685	envelope protein E
470	83.5	4.9	498	2	S11246	LAG-3 protein prec
471	83.5	4.9	527	2	D75127	hypothetical prote
472	83.5	4.9	629	2	AE1525	probable peptidogl
473	83.5	4.9	705	2	S51635	fibroblast growth
474	83.5	4.9	707	2	A38429	keratinocyte growt
475	83.5	4.9	748	2	S41050	fibroblast growth
476	83.5	4.9	750	2	S41051	fibroblast growth
477	83.5	4.9	911	2	I56552	synapse-associated
478	83.5	4.9	987	2	A88746	protein C18F3.2 [l
479	83.5	4.9	1002	2	T19226	hypothetical prote
480	83.5	4.9	1028	2	C88364	protein C18B4.1 [l
481	83.5	4.9	1287	2	T30988	hypothetical prote
482	83.5	4.9	3898	1	GNMVHC	genome polypeptide
483	83	4.9	115	2	B32071	T-cell receptor de
484	83	4.9	233	2	S25747	Ig lambda chain -
485	83	4.9	422	2	B95001	conserved domain p
486	83	4.9	428	2	A27658	pregnancy-specific
487	83	4.9	445	2	A97873	conserved hypochet
488	83	4.9	977	2	S49004	tyrosine kinase Mp
489	83	4.9	1151	2	A45226	integrin alpha-1 c
490	83	4.9	3029	2	S76109	hypothetical prote
491	82.5	4.9	185	2	S37479	T-cell receptor al
492	82.5	4.9	218	2	JCS810	monoclonal antibod
493	82.5	4.9	218	2	B47712	myelin/oligodendro
494	82.5	4.9	229	2	A46527	B-cell-specific me
495	82.5	4.9	230	2	A56210	neu differentiatio
496	82.5	4.9	316	2	C37028	MHC class I histoc
497	82.5	4.9	353	2	S51242	heparin-binding f1
498	82.5	4.9	355	2	I80169	class I histocompa
499	82.5	4.9	356	1	S55437	translation releas
500	82.5	4.9	395	2	D43354	pregnancy-specific
501	82.5	4.9	417	2	A28277	pregnancy-specific
502	82.5	4.9	453	2	B83380	hypothetical prote
503	82.5	4.9	645	2	B43273	heretulin, splice
504	82.5	4.9	651	2	A96781	unknown protein p9
505	82.5	4.9	662	2	I61722	neu differentiatio
506	82.5	4.9	757	1	S48841	secretory componen
507	82.5	4.9	793	2	S59067	penton long fiber
508	82.5	4.9	822	2	S19947	fibroblast growth
509	82.5	4.9	822	2	B49151	fibroblast growth
510	82.5	4.9	942	2	S23251	protein-tyrosine k
511	82.5	4.9	975	2	T42576	probable envelope
512	82.5	4.9	1015	2	T32186	hypothetical prote
513	82.5	4.9	1648	2	S61654	probable membrane
514	82	4.9	147	2	I46625	rearranged T-cell
515	82	4.9	150	2	S36312	T-cell receptor de
516	82	4.9	242	2	S06942	hypothetical prote
517	82	4.9	250	2	H81854	probable zinc-bind
518	82	4.9	261	2	C85681	hypothetical prote
519	82	4.9	324	2	G43354	pregnancy-specific
520	82	4.9	326	2	P43354	pregnancy-specific
521	82	4.9	333	2	A43354	pregnancy-specific
522	82	4.9	335	2	A33514	pregnancy-specific
523	82	4.9	335	2	H43354	pregnancy-specific
524	82	4.9	340	2	T28137	Ig V-region-like B
525	82	4.9	352	2	S09266	Ig alpha chain C r
526	82	4.9	426	2	C55181	pregnancy-specific
527	82	4.9	426	2	S09016	pregnancy-specific
528	82	4.9	426	2	B35334	pregnancy-specific
529	82	4.9	436	2	B55181	pregnancy-specific
530	82	4.9	473	2	T35997	conserved hypochet
531	82	4.9	1086	2	AF1662	cellobiose-phospho
532	82	4.9	1160	2	P88369	protein unc-52 [lm
533	82	4.9	1185	2	D89824	hypothetical prote
534	82	4.9	1898	2	S46216	leukocyte antigen-
535	81.5	4.8	85	2	S08109	carcinoembryonic a
536	81.5	4.8	140	2	C24747	T-cell receptor be
537	81.5	4.8	213	2	S68213	Ig heavy chain (Ma
538	81.5	4.8	235	2	I50610	T-cell surface gly
539	81.5	4.8	314	1	HNWZVM	hemagglutinin prec
540	81.5	4.8	314	1	JQ1793	hemagglutinin prec

541	81.5	4.8	339	2	T28138	Ig V-region-like B	614	79.5	4.7	341	2	S16521	mitosis-specific c
542	81.5	4.8	426	2	A35954	pregnancy-specific	615	79.5	4.7	360	2	S09271	Ig alpha chain C r
543	81.5	4.8	650	1	UC1450	fibroblast growth	616	79.5	4.7	361	2	S68089	actin 2 - Arabidop
544	81.5	4.8	687	2	A49636	soluble vascular e	617	79.5	4.7	374	2	B82227	exodeoxyribonuclea
545	81.5	4.8	699	2	A12686	proteinase II (imp	618	79.5	4.7	483	2	A97744	isocitrate dehydro
546	81.5	4.8	699	2	E97468	dipeptidyl aminope	619	79.5	4.7	495	2	A55181	pregnancy-specific
547	81.5	4.8	707	2	A54846	fibroblast growth	620	79.5	4.7	610	2	A55939	dihydrolipamide S
548	81.5	4.8	822	2	B54846	fibroblast growth	621	79.5	4.7	637	2	T49099	hypothetical prote
549	81.5	4.8	1015	2	T32984	hypothetical prote	622	79.5	4.7	701	2	T17243	endo-beta-N-acetyl
550	81.5	4.8	1462	1	A69809	probable multifunc	623	79.5	4.7	878	2	A83748	starch phosphoryla
551	81.5	4.8	3507	2	T34513	hypothetical prote	624	79.5	4.7	974	2	S34189	neural cell adhesi
552	81	4.8	117	2	S49983	rearranged T-cell	625	79.5	4.7	1209	2	T14357	complement C3 prec
553	81	4.8	139	2	I46630	rearranged T-cell	626	79.5	4.7	1265	1	A37967	Ig lambda chain pr
554	81	4.8	145	2	I46631	biliary glycoprote	627	79.5	4.7	1663	1	C3XR	pregnancy-specific
555	81	4.8	206	2	A40305	hemagglutinin prec	628	79	4.7	118	2	S04519	herregulin precurs
556	81	4.8	315	1	HNWZV	Ig heavy chain - R	629	79	4.7	132	2	PQ0060	vascular cell adhe
557	81	4.8	381	2	I51174	probable advanced	630	79	4.7	210	2	JC4122	aggregran - pig (fr
558	81	4.8	402	2	T09062	T-cell surface gly	631	79	4.7	241	2	D43273	hypothetical prote
559	81	4.8	432	1	RWMQ74	matrix, capsid, nu	632	79	4.7	345	2	A46052	cellular hepatitis
560	81	4.8	438	2	E96545	hypothetical prote	633	79	4.7	370	2	S29139	cyclin A-like prot
561	81	4.8	449	2	A45557	hypothetical prote	634	79	4.7	374	2	A46352	lymphocyte antigen
562	81	4.8	450	2	S25162	gag protein - cell	635	79	4.7	407	2	T08732	77.8k DNA helicase
563	81	4.8	509	2	JC6203	Sf8 binding protei	636	79	4.7	451	2	S71754	probable two-compo
564	81	4.8	767	2	F86383	hypothetical prote	637	79	4.7	502	2	T02746	nematodes resistan
565	81	4.8	823	2	S44873	hypothetical prote	638	79	4.7	567	2	S29498	protein-tyrosine k
566	81	4.8	1433	1	A36724	bcx1loptetidaae F	639	79	4.7	716	1	WZBR6	chromodomain bindi
567	81	4.8	1492	2	T14652	protein U - Yersin	640	79	4.7	741	2	B83265	genome polyprotein
568	81	4.8	1545	2	T14966	phage lambda-relat	641	79	4.7	742	2	F84643	T-cell receptor be
569	81	4.8	1650	2	S53457	dominant autoantig	642	79	4.7	1255	2	T06267	sodium channel bet
570	80.5	4.8	133	2	S57870	T cell receptor Ck	643	79	4.7	1298	2	A48999	Ig kappa chain - s
571	80.5	4.8	142	2	B28344	Vvreb protein prec	644	79	4.7	1315	2	T28679	T-cell receptor al
572	80.5	4.8	366	2	I37523	MHC class I histoc	645	79	4.7	1388	2	T38720	basigin precursor
573	80.5	4.8	426	2	B33258	pregnancy-specific	646	79	4.7	3414	1	GNWVNE	mucin 5AC (clone J
574	80.5	4.8	426	2	A35341	pregnancy-specific	647	79	4.7	136	2	JQ0473	integrin-aseociate
575	80.5	4.8	441	2	T31482	hypothetical prote	648	78.5	4.7	136	2	S36320	inositol monophosp
576	80.5	4.8	551	2	A30342	interleukin-2 rece	649	78.5	4.7	215	2	A57843	class I histocompa
577	80.5	4.8	820	2	S17295	fibroblast growth	650	78.5	4.7	230	2	S33161	class I histocompa
578	80.5	4.8	874	2	T29548	hypothetical prote	651	78.5	4.7	259	2	S57494	class I histocompa
579	80.5	4.8	1216	2	S60613	protein-tyrosine-p	652	78.5	4.7	270	2	S65739	class I histocompa
580	80.5	4.8	1493	2	T10757	MAP kinase kinase	653	78.5	4.7	279	2	S53363	class I histocompa
581	80.5	4.8	1641	2	D82704	conserved hypochet	654	78.5	4.7	334	2	A75363	class I histocompa
582	80.5	4.8	2482	2	I48922	cation-independent	655	78.5	4.7	335	2	S73646	class I histocompa
583	80.5	4.8	2483	1	A49617	insulin-like growt	656	78.5	4.7	355	2	I80171	class I histocompa
584	80	4.7	124	2	F03560	rearranged T-cell	657	78.5	4.7	363	2	S03537	class I histocompa
585	80	4.7	133	2	I46632	T-cell receptor al	658	78.5	4.7	366	2	I37544	MHC class I histoc
586	80	4.7	147	2	S25459	hypothetical prote	659	78.5	4.7	366	2	S42823	MHC class I histoc
587	80	4.7	194	2	T29925	Ig heavy chain V-I	660	78.5	4.7	366	2	B37028	MHC class I histoc
588	80	4.7	218	2	A36040	mitosis-specific c	661	78.5	4.7	407	2	C83589	pregnancy-specific
589	80	4.7	287	2	S71192	cell surface glyco	662	78.5	4.7	419	2	B54312	Ig heavy chain pre
590	80	4.7	304	1	RKCH7	MHC class I histoc	663	78.5	4.7	568	2	A34891	E-selectin precurs
591	80	4.7	365	2	A45847	Ig heavy chain pre	664	78.5	4.7	612	2	B42755	DNA ligase (ATP) (
592	80	4.7	549	2	S04845	aldenhyde:ferredoxi	665	78.5	4.7	787	2	A29066	probable lipoprote
593	80	4.7	684	2	F97148	neuronal leucine-r	666	78.5	4.7	916	2	S73892	cadherin 4 precurs
594	80	4.7	707	2	JC7763	probable secreted	667	78.5	4.7	1059	2	T22545	hypothetical prote
595	80	4.7	748	2	T37097	surface-array prote	668	78.5	4.7	1188	1	A57064	sex factor aggrega
596	80	4.7	893	2	A37284	hypothetical prote	669	78.5	4.7	1243	2	S60138	hyperplastic discs
597	80	4.7	939	2	A82275	myosin-binding pro	670	78.5	4.7	1609	2	S25345	probable tenascin
598	80	4.7	999	2	S72267	fibronectin - Afri	671	78.5	4.7	2895	2	T08437	hypothetical prote
599	80	4.7	1123	2	S36846	hypothetical prote	672	78.5	4.7	4006	2	T09070	T-cell receptor al
600	80	4.7	1582	2	T15308	T-cell receptor de	673	78.5	4.7	95	2	B98068	B-lymphocyte activ
601	80	4.7	2481	2	A43908	T-cell receptor al	674	78.5	4.7	121	2	A29080	pregnancy-specific
602	80	4.7	3488	2	T34418	rearranged T-cell	675	78	4.6	1309	2	C54312	Fil-1S protein pre
603	79.5	4.7	104	2	S36305	rearranged T-cell	676	78	4.6	335	2	S41101	putrescine-binding
604	79.5	4.7	114	2	JH0341	Ig lambda chain -	677	78	4.6	362	2	B71032	fasciclin III prec
605	79.5	4.7	135	2	S36298	Ig lambda chain -	678	78	4.6	367	2	A33378	Ig mu chain - shee
606	79.5	4.7	137	2	C45893	rearranged T-cell	679	78	4.6	367	2	AE3303	novel antigen rece
607	79.5	4.7	140	2	I46638	rearranged T-cell	680	78	4.6	392	2	S25705	killer cell inhibi
608	79.5	4.7	147	2	I46623	Ig lambda chain -	681	78	4.6	617	2	B64734	glycoprotein 350/2
609	79.5	4.7	232	2	S25756	fibroblast growth	682	78	4.6	684	2	S60266	
610	79.5	4.7	254	2	C42691	B7 protein - red-c	683	78	4.6	841	2	JC5894	
612	79.5	4.7	313	2	I36958	MHC class chain - c	685	78	4.6	886	2	S29605	
613	79.5	4.7	335	2	S09275	Ig alpha chain C r	686	78	4.6				

687	78	4.6	1185	2	A42404	collagen adhesin -
688	78	4.6	1203	2	T04294	leukocyte common a
689	78	4.6	1273	1	TDRIT	typic protein - bli
690	78	4.6	3848	2	T17414	calo protein - fru
691	78	4.6	4116	2	T13719	Ig lambda chain -
692	77.5	4.6	103	2	S36067	T-cell receptor al
693	77.5	4.6	104	2	G24402	Ig lambda chain -
694	77.5	4.6	122	2	S16439	T-cell receptor al
695	77.5	4.6	134	2	A45893	Ig lambda chain -
696	77.5	4.6	182	2	I83053	T-cell receptor al
697	77.5	4.6	226	2	S25745	pregnancy-specific
698	77.5	4.6	227	2	A33937	Ig lambda chain -
699	77.5	4.6	235	2	S25758	Ig light chain (13
700	77.5	4.6	240	2	JC4121	pregnancy-specific
701	77.5	4.6	288	2	S26690	Ig heavy chain VDJ
702	77.5	4.6	295	2	A37412	T-cell receptor de
703	77.5	4.6	332	2	UN0067	pregnancy-specific
704	77.5	4.6	333	1	S42102	MHC class I histoc
705	77.5	4.6	364	2	S59931	glycerophosphodier
706	77.5	4.6	364	2	S59932	glycerophosphodier
707	77.5	4.6	364	2	S59933	glycerophosphodier
708	77.5	4.6	364	2	A43576	glycerophosphodier
709	77.5	4.6	364	2	S59934	glycerophosphodier
710	77.5	4.6	420	2	H84182	hypothetical prote
711	77.5	4.6	496	2	S60686	envelope protein E
712	77.5	4.6	509	2	S17597	Ig delta chain (W1
713	77.5	4.6	537	2	A46611	myosin-binding pro
714	77.5	4.6	542	2	S49219	fiber protein - ca
715	77.5	4.6	662	2	T16525	hypothetical prote
716	77.5	4.6	704	2	A48040	mepirin A (BC 3.4.2
717	77.5	4.6	1009	2	T18533	Crylic toxin-bindi
718	77.5	4.6	1036	2	B69368	hypothetical prote
719	77.5	4.6	1047	2	T41343	probable translati
720	77.5	4.6	1141	2	B89824	hypothetical prote
721	77.5	4.6	1997	1	S12050	protein-tyrosine-p
722	77	4.6	95	2	D95201	hypothetical prote
723	77	4.6	113	2	JH0340	T-cell receptor al
724	77	4.6	135	2	S26512	T-cell receptor de
725	77	4.6	146	2	S36323	hypothetical prote
726	77	4.6	309	2	T15747	hypothetical prote
727	77	4.6	331	2	T31517	hypothetical prote
728	77	4.6	356	2	F71624	riifin PFB0060w - m
729	77	4.6	396	2	T45033	hypothetical prote
730	77	4.6	400	1	A39822	leukostialin precu
731	77	4.6	403	2	I52590	m3-B isoform - mo
732	77	4.6	430	2	T28143	tepasin 1 homolog,
733	77	4.6	433	2	T17289	hypothetical prote
734	77	4.6	462	2	A41158	dipeptidyl-peptida
735	77	4.6	496	2	A43383	envelope glycoprot
736	77	4.6	590	2	I56526	interleukin 1 rece
737	77	4.6	630	2	T51281	beta-D-glucan exoh
738	77	4.6	639	2	T20772	hypothetical prote
739	77	4.6	661	2	B54078	methyI-accepting c
740	77	4.6	680	2	JC5895	killer cell inhibi
741	77	4.6	690	2	G84638	hypothetical prote
742	77	4.6	800	2	AB1129	internatin A [impo
743	77	4.6	846	2	T19179	hypothetical prote
744	77	4.6	1666	2	T38393	clathrin heavy cha
745	77	4.6	2491	1	A28372	insulin-like growt
746	76.5	4.5	114	2	I38316	T-cell receptor de
747	76.5	4.5	115	2	S03513	T-cell receptor de
748	76.5	4.5	120	2	S36306	rearranged T-cell
749	76.5	4.5	151	2	I46626	flagellar hook ass
750	76.5	4.5	239	2	G97165	OX-45 membrane gly
751	76.5	4.5	240	2	S01299	T-cell surface gly
752	76.5	4.5	240	2	A39016	hypothetical 29.3k
753	76.5	4.5	255	2	JQ1240	GRSAG protein 9u
754	76.5	4.5	296	2	B39581	daunorubicin resis
755	76.5	4.5	318	2	H75157	Pc gamma (Igg) rec
756	76.5	4.5	336	2	I48471	oligopeptide abc t
757	76.5	4.5	477	2	H75026	hypothetical prote
758	76.5	4.5	530	2	T18596	probable purine nu
759	76.5	4.5	742	2	S38093	

760	76.5	4.5	771	2	A83348	probable aldehyde
761	76.5	4.5	874	2	C84513	Mutator-like trans
762	76.5	4.5	1110	2	T19673	hypothetical prote
763	76.5	4.5	1138	2	S24614	myosin-binding pro
764	76.5	4.5	1350	2	AF2005	RNA polymerase bet
765	76.5	4.5	1365	2	T30198	alkaline phosphata
766	76.5	4.5	1832	2	T31113	mucin-like glycopr
767	76	4.5	120	2	C26945	T-cell receptor de
768	76	4.5	133	2	P24402	T-cell receptor al
769	76	4.5	141	2	S36318	T-cell receptor de
770	76	4.5	145	2	S25743	Ig lambda chain -
771	76	4.5	149	2	S36317	T-cell receptor de
772	76	4.5	323	2	S06946	Fc gamma (Igg) rec
773	76	4.5	341	2	S26686	CAMP response elem
774	76	4.5	360	2	A27638	MHC class I histoc
775	76	4.5	362	2	I72755	HLA-B*5602 - human
776	76	4.5	362	2	I72754	HLA-B*5601 - human
777	76	4.5	365	2	I38439	MHC class I histoc
778	76	4.5	366	2	I81231	lymphocyte antigen
779	76	4.5	400	2	AD3364	probable acyl-CoA
780	76	4.5	401	2	AG3552	branched-chain ami
781	76	4.5	415	2	AB3637	alpha-methylacyl-C
782	76	4.5	441	2	H96817	hypothetical prote
783	76	4.5	443	2	A96818	hypothetical prote
784	76	4.5	446	2	F84451	probable uridylyl
785	76	4.5	457	1	RMNST4	T-cell surface gly
786	76	4.5	478	2	AP1758	chitinase and chit
787	76	4.5	492	2	PC4408	protein E - Tick-b
788	76	4.5	562	2	A65166	hypothetical 63.2k
789	76	4.5	562	2	B91194	probable enzyme [1
790	76	4.5	569	2	C86041	probable enzyme y1
791	76	4.5	602	2	T16135	hypothetical prote
792	76	4.5	649	2	T32755	hypothetical prote
793	76	4.5	800	2	S37387	internatin A precu
794	76	4.5	959	1	P2XR13	outer capsid prote
795	76	4.5	1032	2	T34433	hypothetical prote
796	76	4.5	1497	2	I49607	procollagen type V
797	76	4.5	2232	2	T34434	hypothetical prote
798	76	4.5	3716	2	E70969	probable PPG prote
799	76	4.5	4660	2	T43737	gp330 protein prec
800	75.5	4.5	52558	2	S22558	Ig heavy chain V r
801	75.5	4.5	116	2	H32536	T-cell receptor al
802	75.5	4.5	275	2	PS0402	basigin type III -
803	75.5	4.5	283	2	F87183	probable exported
804	75.5	4.5	297	2	AG2955	hypothetical prote
805	75.5	4.5	297	2	F98327	hypothetical prote
806	75.5	4.5	312	2	H64560	probable tetraacyl
807	75.5	4.5	342	2	A45966	Ig alpha chain C r
808	75.5	4.5	366	2	I37527	MHC class I histoc
809	75.5	4.5	371	2	A53908	brevican precursor
810	75.5	4.5	398	2	A39371	Ig V-region-like B
811	75.5	4.5	484	2	B64481	hypothetical prote
812	75.5	4.5	549	2	G66618	dipeptide ABC tran
813	75.5	4.5	607	2	A95122	Th552, relaxase l
814	75.5	4.5	705	1	CIHURB	complement subcomp
815	75.5	4.5	742	2	A49340	alcohol dehydrogen
816	75.5	4.5	769	2	E90158	AAA family ATPase
817	75.5	4.5	796	2	T20393	hypothetical prote
818	75.5	4.5	937	2	A45082	neurotrophic recep
819	75.5	4.5	1042	2	AF0739	exodeoxyribonuclea
820	75.5	4.5	1294	2	T04278	hypothetical prote
821	75.5	4.5	1662	2	T01893	hypothetical prote
822	75.5	4.5	1902	2	C97702	cell surface antlg
823	75	4.4	132	1	RMMSAV	T-cell receptor al
824	75	4.4	141	2	S38389	T-cell receptor be
825	75	4.4	233	2	S25744	Ig lambda chain -
826	75	4.4	234	2	S01320	Ig kappa chain pre
827	75	4.4	238	2	D90876	major tail protein
828	75	4.4	252	2	H72554	probable Rieseke pr
829	75	4.4	262	2	C85692	probable tail comp
830	75	4.4	301	2	AC3476	probable proteinas
831	75	4.4	335	2	B33251	nonpeptide cross-
832	75	4.4	346	2	C81088	alcohol dehydrogen

833	75	4.4	360	2	AE1931	hypotheoretical prote
834	75	4.4	362	2	I37120	MHC class I histoc
835	75	4.4	362	2	B30345	MHC class I histoc
836	75	4.4	362	2	I37522	MHC class I histoc
837	75	4.4	362	2	I61904	MHC class I histoc
838	75	4.4	362	2	I54457	MHC class I lympho
839	75	4.4	362	2	A30345	MHC class I histoc
840	75	4.4	367	2	H65132	hypotheoretical 44.3
841	75	4.4	391	1	MHUBT	Ig mu heavy chain
842	75	4.4	396	2	C95088	S-adenosylmethionyl
843	75	4.4	396	2	G97955	methionine adenosyl
844	75	4.4	450	1	FOLJPP	gag polyprotein -
845	75	4.4	450	2	S23819	Ras inhibitor (clo
846	75	4.4	471	2	B38637	hypotheoretical prote
847	75	4.4	483	2	A69745	envelope glycoprot
848	75	4.4	496	2	PQ0508	hypotheoretical prote
849	75	4.4	496	2	E90181	colicin (partial)
850	75	4.4	507	2	AE0473	hypotheoretical prote
851	75	4.4	552	2	T01142	L-lactate permease
852	75	4.4	563	2	A70038	poly(3)-hydroxybuty
853	75	4.4	589	2	A34341	inner membrane cop
854	75	4.4	600	2	A82043	hypotheoretical prote
855	75	4.4	630	2	F85074	MC288 homolog D09
856	75	4.4	632	2	S73431	luciferin-binding
857	75	4.4	673	2	S46520	Delta-4 protein -
858	75	4.4	686	2	JC7569	hypotheoretical prote
859	75	4.4	808	2	T23129	Ca2+-transporting
860	75	4.4	997	2	A40812	Ca2+-transporting
861	75	4.4	999	2	A34307	endo-1,4-beta-xyla
862	75	4.4	1042	2	B40812	genome, polyprotein
863	75	4.4	1234	2	S72640	synaptic scafoldi
864	75	4.4	1241	2	S26373	probable cell surf
865	75	4.4	1277	2	T14152	probable peptidogl
866	75	4.4	1622	2	AE1717	aggregran precursor
867	75	4.4	2109	1	I50421	aggregran precursor
868	75	4.4	2134	2	A28452	aggregran precursor
869	75	4.4	2132	1	A55182	aggregran precursor
870	75	4.4	2132	1	A55182	aggregran precursor
871	75	4.4	2415	1	A39086	aggregran precursor
872	75	4.4	3216	2	C90538	hypotheoretical prote
873	75	4.4	3263	2	E82410	large repetitive p
874	75	4.4	3624	2	AD0835	T-cell receptor al
875	74.5	4.4	115	2	A24891	T-cell receptor be
876	74.5	4.4	131	2	PQ0059	T-cell receptor al
877	74.5	4.4	133	2	S57885	T-cell receptor al
878	74.5	4.4	135	1	RMHDAV	YbDQ protein - Bsc
879	74.5	4.4	142	1	E64794	hypotheoretical prote
880	74.5	4.4	142	2	P90709	hypotheoretical prote
881	74.5	4.4	142	2	B85560	hypotheoretical prote
882	74.5	4.4	208	2	B49444	Ig lambda chain (N
883	74.5	4.4	212	2	C33258	pregnancy-specific
884	74.5	4.4	235	2	AD1735	hypotheoretical prote
885	74.5	4.4	234	2	T05381	hypotheoretical prote
886	74.5	4.4	345	2	C72760	probable heme expo
887	74.5	4.4	348	2	I50107	MHC class I histoc
888	74.5	4.4	361	2	B90451	hypotheoretical prote
889	74.5	4.4	366	1	HLHMW3	MHC class I histoc
890	74.5	4.4	377	2	A49885	MHC class I histoc
891	74.5	4.4	445	2	S43492	surface antigen -
892	74.5	4.4	476	2	A10189	exosome-ribonuclea
893	74.5	4.4	503	2	AB1933	hypotheoretical prote
894	74.5	4.4	625	2	T16777	hypotheoretical prote
895	74.5	4.4	652	2	G96560	DNA-directed RNA p
896	74.5	4.4	717	2	B32838	ERs domain protein
897	74.5	4.4	732	2	A43315	interleukin-4 rece
898	74.5	4.4	810	1	A33380	neurotrophic recep
899	74.5	4.4	943	2	B45082	Tomb-dependent rec
900	74.5	4.4	946	2	B87316	mitotic control pr
901	74.5	4.4	1000	2	JB0110	cellobiose-phospho
902	74.5	4.4	1086	2	AH1290	hypotheoretical prote
903	74.5	4.4	1302	2	AC2574	probable membrane
904	74.5	4.4	1333	2	S63403	hypotheoretical prote
905	74.5	4.4	1356	2	T16718	hypotheoretical prote
906	74.5	4.4	1446	2	T13018	hypotheoretical prote
907	74.5	4.4	1615	2	C75551	glutamate synthase
908	74.5	4.4	2143	2	G96595	hypotheoretical prote
909	74.5	4.4	3890	2	C89921	hypotheoretical prote
910	74.5	4.4	4436	2	B71086	hypotheoretical prote
911	74	4.4	115	2	A30583	T-cell receptor de
912	74	4.4	130	2	S08079	Ig kappa chain pre
913	74	4.4	143	2	S36321	T-cell receptor de
914	74	4.4	145	2	S36299	T-cell receptor de
915	74	4.4	217	2	UE0246	Ig lambda chain NI
916	74	4.4	264	2	T26976	hypotheoretical prote
917	74	4.4	270	1	S77085	molybdate-binding
918	74	4.4	318	2	C71197	probable ATP-bind
919	74	4.4	327	2	P87544	UDP-glucose 4-epim
920	74	4.4	330	2	AE3119	ABC transporter, s
921	74	4.4	341	2	S20827	CAMP response elem
922	74	4.4	351	2	S78042	Ig mu chain C regi
923	74	4.4	353	2	C86932	conserved hypochet
924	74	4.4	354	2	S24436	class I histocompa
925	74	4.4	362	2	I56130	HLA-B*5401 - human
926	74	4.4	362	2	I59633	MHC HLA-B transmem
927	74	4.4	362	2	I72753	HLA-B*5502 - human
928	74	4.4	362	2	S24434	class I histocompa
929	74	4.4	362	2	I72752	HLA-B*5501 - human
930	74	4.4	362	2	I56133	MHC class I proteol
931	74	4.4	365	2	B95260	recf proteol (limp
932	74	4.4	365	2	B98125	recombination prot
933	74	4.4	387	2	B98168	periplasmic-iron-b
934	74	4.4	425	2	E71982	isocitrate dehydro
935	74	4.4	430	2	S50981	probable membrane
936	74	4.4	487	2	AD3643	adhesion aid-I (im
937	74	4.4	509	2	JC5288	SHP substrate-1 pr
938	74	4.4	513	2	JC5289	SHP substrate-1 pr
939	74	4.4	517	2	B87644	4-coumarate-CoA li
940	74	4.4	555	2	T47330	hypotheoretical prote
941	74	4.4	570	2	T47573	peptide transport-
942	74	4.4	617	2	A90644	probable membrane
943	74	4.4	617	2	A85495	probable membrane
944	74	4.4	626	2	I38618	zinc finger proteol
945	74	4.4	628	2	T51283	glucan 1,3-beta-gl
946	74	4.4	635	2	JC5896	killer cell inhibi
947	74	4.4	640	2	B84478	probable replicati
948	74	4.4	642	2	S58154	hypotheoretical prote
949	74	4.4	666	2	H89581	protein dim-1 (limp
950	74	4.4	708	2	T19474	hypotheoretical prote
951	74	4.4	809	2	AG0859	outer membrane ush
952	74	4.4	1020	2	A46405	C protein alpha an
953	74	4.4	1144	2	D97227	pyruvate carboxyla
954	74	4.4	1251	2	T21389	hypotheoretical prote
955	74	4.4	1452	1	S17670	protein-tyrosine-p
956	74	4.4	1537	2	JC4172	DNA (cytosine-5-)-
957	74	4.4	1763	2	T17465	riifamycin polyketi
958	74	4.4	3412	1	GNMWTB	genome polyprotein
959	74	4.4	106	2	PL0267	Ig kappa chain V r
960	73.5	4.4	108	1	KVRH85	Ig lambda chain V r
961	73.5	4.4	111	1	L6RH8T	Ig lambda chain V-
962	73.5	4.4	111	2	JH0339	T-cell receptor al
963	73.5	4.4	229	2	A20969	Ig kappa chain pre
964	73.5	4.4	245	2	T18609	hypotheoretical prote
965	73.5	4.4	246	2	S38950	Ig gamma chain - m
966	73.5	4.4	253	2	T15475	hypotheoretical prote
967	73.5	4.4	257	2	PS0401	basigin type II -
968	73.5	4.4	271	2	S43512	GP42/Baafign prote
969	73.5	4.4	273	2	UX0107	basigin precursor
970	73.5	4.4	283	1	PCMSG1	Fc gamma (1g) rec
971	73.5	4.4	291	2	T30488	hypotheoretical prote
972	73.5	4.4	304	2	B88746	protein C18F3.3 (l
973	73.5	4.4	310	2	JL0119	Fc gamma (1g) rec
974	73.5	4.4	316	2	H71231	molybdopterin bios
975	73.5	4.4	325	2	I54449	MHC class I HLA-Cx
976	73.5	4.4	330	2	A40071	Fc gamma (1g) rec
977	73.5	4.4	330	2	I49660	Fc-gamma-1/gamma-2
978	73.5	4.4	339	2	JC7509	glycoprotein VI-1

979	73.5	4.4	348	2	S09273	Ig alpha chain C r	1052	73	4.3	362	2	I84490	lymphocyte antigen
980	73.5	4.4	351	2	B34595	pregnancy-specific	1053	73	4.3	362	2	A45880	MHC class I histoc
981	73.5	4.4	351	2	A97064	D-mannanase hydrol	1054	73	4.3	362	2	I54442	MHC class I histoc
982	73.5	4.4	357	2	D82337	UDP-N-acetylenolpy	1055	73	4.3	365	2	I37482	MHC class I histoc
983	73.5	4.4	352	2	S68090	actin 8 - Arabidop	1056	73	4.3	378	2	S41870	surface antigen -
984	73.5	4.4	366	2	I68712	MHC class I histoc	1057	73	4.3	426	2	C72166	A22R protein - var
985	73.5	4.4	366	2	F72062	hypothetical prote	1058	73	4.3	489	2	T09151	glutathione-dialuf
986	73.5	4.4	366	2	A86561	CT449 hypothetical	1059	73	4.3	499	2	E86782	D-alanine activati
987	73.5	4.4	400	2	T34363	hypothetical prote	1060	73	4.3	507	2	A48661	cystathionine beta
988	73.5	4.4	404	2	A46480	Fe gamma (196) rec	1061	73	4.3	508	2	B91250	hypothetical prote
989	73.5	4.4	408	2	F81252	NADH2 dehydrogenas	1062	73	4.3	521	2	B84746	hypothetical prote
990	73.5	4.4	427	2	F64064	colb protein - Hae	1063	73	4.3	580	2	AE1088	ABC transporter, A
991	73.5	4.4	446	2	S40295	Ig gamma-2a chain	1064	73	4.3	615	2	T20839	hypothetical prote
992	73.5	4.4	451	2	T30603	perlecan homolog 2	1065	73	4.3	681	2	A45055	glutamine-fructose
993	73.5	4.4	482	2	T22754	hypothetical prote	1066	73	4.3	685	2	TC7570	Delta-4 protein -
994	73.5	4.4	551	2	G84301	hypothetical prote	1067	73	4.3	694	2	F97279	TPR-repeat-contain
995	73.5	4.4	554	2	C70512	hypothetical prote	1068	73	4.3	866	2	B85075	probable achilla tr
996	73.5	4.4	555	2	D71444	probable thioester	1069	73	4.3	885	2	S42841	T16612.1 protein -
997	73.5	4.4	568	2	A89958	acetyl-CoA synthet	1070	73	4.3	913	2	IJCCHR	R-cadherin precurs
998	73.5	4.4	650	2	S22835	alpha-agglutinin -	1071	73	4.3	954	2	AI0438	probable exported
999	73.5	4.4	659	2	A85854	hypothetical prote	1072	73	4.3	974	1	URHNP	peptidylglycine mo
1000	73.5	4.4	659	2	G91009	colicin I receptor	1073	73	4.3	977	2	I45877	protein-tyrosine k
1001	73.5	4.4	663	1	QREKIC	colicin I receptor	1074	73	4.3	998	2	H75005	ATP-dependent prot
1002	73.5	4.4	666	2	D82511	1,4-alpha-glucan b	1075	73	4.3	1071	2	B84062	hypothetical prote
1003	73.5	4.4	721	2	T05815	hypothetical prote	1076	73	4.3	1115	2	T29012	hypothetical prote
1004	73.5	4.4	737	2	T46243	hypothetical prote	1077	73	4.3	1137	2	E86708	pyruvate carboxyla
1005	73.5	4.4	743	2	D64062	GTP diaphosphokinas	1078	73	4.3	1144	2	AB1983	probable DNA-direc
1006	73.5	4.4	780	2	A34102	von Willebrand fac	1079	73	4.3	1177	2	T16594	hypothetical prote
1007	73.5	4.4	785	2	S54016	SOK2 protein - yea	1080	73	4.3	1199	2	T23005	hypothetical prote
1008	73.5	4.4	790	2	I51638	F-cadherin - Afri	1081	73	4.3	1289	2	C70044	probable phosphoe
1009	73.5	4.4	794	2	T36972	probable membrane	1082	73	4.3	1293	2	E85557	enterobactin synth
1010	73.5	4.4	813	1	A49123	fibroblast growth	1083	73	4.3	1293	2	A90707	hypothetical prote
1011	73.5	4.4	868	2	D86349	hypothetical prote	1084	73	4.3	1311	2	T33757	probable ABC trans
1012	73.5	4.4	886	2	E75625	hypothetical prote	1085	73	4.3	1407	1	T00558	probable protein-l
1013	73.5	4.4	891	2	T19915	hypothetical prote	1086	73	4.3	1437	2	T31093	probable cancer tumo
1014	73.5	4.4	899	1	GNMWM	fibronectin-binding	1087	73	4.3	1452	1	S17669	protein-tyrosine-p
1015	73.5	4.4	1117	2	S33851	pol polyprotein -	1088	73	4.3	1484	2	T42632	brest cancer tumo
1016	73.5	4.4	1127	1	E71156	endopeptidase Ia h	1089	73	4.3	1615	2	BA9502	protein-tyrosine-p
1017	73.5	4.4	1133	1	GNMUR	M polypeptide prec	1090	73	4.3	1714	1	S18644	multifunctional am
1018	73.5	4.4	1133	2	S12597	M polypeptide prec	1091	73	4.3	1767	2	A49502	protein-tyrosine-p
1019	73.5	4.4	1166	2	T28680	fibritrogen-binding	1092	73	4.3	2118	2	S72705	myocerosate synth
1020	73.5	4.4	1259	2	H65233	yeftN protein - Esc	1093	73	4.3	2505	1	XVRTFA	enoyl-l-acyl-carile
1021	73.5	4.4	1293	1	YGECEP	enterobactin synth	1094	73	4.3	2550	2	B53435	vesicular transpor
1022	73.5	4.4	1507	2	T97106	large chain of NAD	1095	73	4.3	2824	2	T23759	hypothetical prote
1023	73.5	4.4	2218	2	B84683	hypothetical prote	1096	73	4.3	3947	2	T52486	ferrichrome sidero
1024	73.5	4.4	2761	2	T21064	hypothetical prote	1097	73	4.3	15281	2	S41309	cytolsporin synth
1025	73.5	4.4	2899	2	T21546	hypothetical prote	1098	72.5	4.3	104	2	S36064	Ig lambda chain -
1026	73.5	4.4	2915	2	G78767	protein F36A2.13 l	1099	72.5	4.3	110	2	S23368	T-cell receptor al
1027	73.5	4.4	3097	2	T28635	glutamate synthase	1100	72.5	4.3	110	2	S22897	T-cell receptor al
1028	73	4.3	107	2	B45722	anti-glycoprotein	1101	72.5	4.3	111	1	L6HULT	Ig lambda chain V-
1029	73	4.3	113	2	I46637	rearranged T-cell	1102	72.5	4.3	112	1	L1HUMA	Ig lambda chain V-
1030	73	4.3	113	2	B49041	T-cell receptor al	1103	72.5	4.3	114	2	T38315	T-cell receptor be
1031	73	4.3	120	2	B25429	T-cell receptor be	1104	72.5	4.3	114	2	I38314	T-cell receptor be
1032	73	4.3	126	2	B46538	Ig heavy chain, me	1105	72.5	4.3	115	2	S03511	T-cell receptor be
1033	73	4.3	131	1	L6HTEB	Ig lambda chain pr	1106	72.5	4.3	133	2	S03510	T-cell receptor be
1034	73	4.3	135	2	S00388	T-cell receptor ga	1107	72.5	4.3	133	2	A25777	T-cell receptor be
1035	73	4.3	162	2	E71131	hypothetical prote	1108	72.5	4.3	135	1	RKHUVY	T-cell receptor be
1036	73	4.3	173	2	T27373	peptidylprolyl iso	1109	72.5	4.3	136	2	S57877	T cell receptor CK
1037	73	4.3	175	2	I38408	neu differentiatio	1110	72.5	4.3	135	2	I46635	rearranged T-cell
1038	73	4.3	186	2	I61783	sodium channel bet	1111	72.5	4.3	140	2	PH0132	Ig lambda chain pr
1039	73	4.3	210	2	I49294	CD7 antigen - mous	1112	72.5	4.3	224	2	B81783	hypothetical prote
1040	73	4.3	213	2	S21066	Ig lambda chain V	1113	72.5	4.3	233	2	TH0372	42k surface glycop
1041	73	4.3	244	2	S12328	Ig heavy chain C r	1114	72.5	4.3	249	2	S69340	Ig heavy chain VHI
1042	73	4.3	247	2	AF0869	probable fibribrial	1115	72.5	4.3	250	2	D83835	hypothetical prote
1043	73	4.3	251	2	T15495	hypothetical prote	1116	72.5	4.3	307	1	RWMSBC	T-cell receptor be
1044	73	4.3	253	2	G97267	PHP superfamily hy	1117	72.5	4.3	312	2	T33344	UDP-glucose 4-epim
1045	73	4.3	267	1	RWMSBC	T-cell receptor al	1118	72.5	4.3	334	2	D83788	hypothetical prote
1046	73	4.3	354	2	B82850	fibmbrial adhesin p	1119	72.5	4.3	365	2	JH0537	MHC class I histoc
1047	73	4.3	362	1	H1HUB8	MHC class I histoc	1120	72.5	4.3	366	2	I54430	MHC class I histoc
1048	73	4.3	362	2	A45834	MHC class I histoc	1121	72.5	4.3	366	2	I61866	MHC class I histoc
1049	73	4.3	362	2	I61907	MHC class I histoc	1122	72.5	4.3	366	2	I56034	gene HLA-C protein
1050	73	4.3	362	2	A45850	MHC class I histoc	1123	72.5	4.3	408	2	S76830	hypothetical prote
1051	73	4.3	362	2	I81233	lymphocyte antigen	1124	72.5	4.3	416	1	KIVKGL	phosphoglycerate k

1125	72.5	4.3	426	2	D42519	A20R protein - vac	1198	72	4.3	997	2	S23444	Ca2+-transporting
1126	72.5	4.3	426	2	T37408	probable 49.1K pro	1199	72	4.3	997	2	S04651	Ca2+-transporting
1127	72.5	4.3	432	2	T43476	hypothetical prote	1200	72	4.3	997	2	B31982	Ca2+-transporting
1128	72.5	4.3	460	2	T38608	hypothetical prote	1201	72	4.3	1042	1	PWRBMC	Ca2+-transporting
1129	72.5	4.3	468	1	VGBEH	glycoprotein gp13	1202	72	4.3	1042	2	A31981	Ca2+-transporting
1130	72.5	4.3	471	1	PABCA	alkaline phosphat	1203	72	4.3	1042	2	S04652	Ca2+-transporting
1131	72.5	4.3	481	2	S62427	G-protein signalin	1204	72	4.3	1042	2	A31981	Ca2+-transporting
1132	72.5	4.3	491	1	IUBCP	p-cadherin - bovin	1205	72	4.3	1043	2	A31982	Ca2+-transporting
1133	72.5	4.3	502	1	A83938	lipopolysaccharide	1206	72	4.3	1135	1	GNVOH	M polyprotein - Ha
1134	72.5	4.3	503	2	JC5287	SNP substrate-1 pr	1207	72	4.3	1135	1	GNVOH	M polyprotein - Ha
1135	72.5	4.3	533	2	T34458	hypothetical prote	1208	72	4.3	1218	2	AD0837	ABC transport prot
1136	72.5	4.3	553	1	H46329	cell fusion glycop	1209	72	4.3	1218	2	T30293	ABC transport prot
1137	72.5	4.3	558	2	S57830	glucose-6-phosphat	1210	72	4.3	1289	2	B90098	RNA polymerase III
1138	72.5	4.3	559	2	S41806	glucose-6-phosphat	1211	72	4.3	1306	2	S25370	MSB2 protein - yea
1139	72.5	4.3	612	2	B84936	RNA polymerase sig	1212	72	4.3	1408	2	H69068	cell surface glyco
1140	72.5	4.3	619	2	A43361	Res-related trans	1213	72	4.3	1695	2	A56921	kinesin family pro
1141	72.5	4.3	641	2	G85043	hypothetical prote	1214	72	4.3	2090	2	S26058	probable transform
1142	72.5	4.3	694	2	G01161	thymopietin alpha	1215	72	4.3	2142	1	ZLVNPV	genome polyprotein
1143	72.5	4.3	723	2	T30094	hypothetical prote	1216	72	4.3	2142	2	T14328	protein-tyrosine-p
1144	72.5	4.3	780	1	S43859	Alpase - Sulfolobu	1217	72	4.3	2302	2	MMWYTD	nonstructural poly
1145	72.5	4.3	820	2	T14879	hypothetical prote	1218	72	4.3	2482	1	MMWYTD	probable RTX fami
1146	72.5	4.3	867	2	AD1856	hypothetical prote	1219	72	4.3	5291	2	P90696	hypothetical prote
1147	72.5	4.3	899	2	B75018	hypothetical prote	1220	72	4.3	5291	2	P90696	T-cell receptor al
1148	72.5	4.3	923	2	S09583	peptidylglycine mo	1221	71.5	4.2	101	2	S29588	Ig kappa chain V r
1149	72.5	4.3	976	1	TVHUKT	protein-tyrosine k	1222	71.5	4.2	102	2	S22891	T-cell receptor al
1150	72.5	4.3	980	2	A38523	genome polyprotein	1223	71.5	4.2	113	2	S03410	Ig kappa chain pre
1151	72.5	4.3	1088	1	PFRFGA	platelet-derived g	1224	71.5	4.2	139	1	RMH07A	T-cell receptor al
1152	72.5	4.3	1131	2	T15787	hypothetical prote	1225	71.5	4.2	142	2	S36310	T-cell receptor de
1153	72.5	4.3	1143	1	S46122	SNF2 protein homol	1226	71.5	4.2	148	2	A32536	T-cell receptor al
1154	72.5	4.3	1663	1	C3MS	complement C3 prec	1227	71.5	4.2	155	2	S58178	T cell antigen rec
1155	72.5	4.3	1707	2	AH2085	two-component hybr	1228	71.5	4.2	155	2	S71257	major latex protei
1156	72.5	4.3	2201	2	AH0095	probable sideropho	1229	71.5	4.2	246	2	PC4397	mucin 3 T10 - huma
1157	72.5	4.3	3283	2	AC1018	large repetitive p	1230	71.5	4.2	255	1	S48146	mucin 1 precursor,
1158	72	4.3	111	2	S26255	T-cell receptor be	1231	71.5	4.2	259	1	S60617	hypothetical prote
1159	72	4.3	111	2	S26255	T-cell receptor be	1232	71.5	4.2	270	2	G84163	hypothetical prote
1160	72	4.3	111	2	S09063	Ig kappa chain V-J	1233	71.5	4.2	291	2	J01562	hypothetical prote
1161	72	4.3	136	2	S36304	T-cell receptor de	1234	71.5	4.2	299	2	I46590	CD80 precursor - r
1162	72	4.3	138	2	PN0538	Ig heavy chain V r	1235	71.5	4.2	329	2	JC5168	UDPglucose 4-epime
1163	72	4.3	144	2	A27577	T-cell receptor al	1236	71.5	4.2	337	2	S65022	glucan endo-1,3-be
1164	72	4.3	171	2	S38237	hypothetical prote	1237	71.5	4.2	345	2	I68749	MHC class I lympho
1165	72	4.3	259	1	P69678	involved in polyke	1238	71.5	4.2	352	2	G81921	hypothetical prote
1166	72	4.3	281	2	S34626	translaton elonga	1239	71.5	4.2	354	2	G64086	glycerophosphodis
1167	72	4.3	285	2	S36903	Fe gamma (Irg) rec	1240	71.5	4.2	355	1	S76914	translation releas
1168	72	4.3	286	2	I46021	Fe-gamma receptor	1241	71.5	4.2	366	2	I37526	MHC class I histoc
1169	72	4.3	323	1	PEPLBJ	penicillopepsin (E	1242	71.5	4.2	366	2	I72113	MHC histocompatib
1170	72	4.3	333	2	JC7713	ankyrin-repeat pro	1243	71.5	4.2	366	2	I59622	lymphocyte antigen
1171	72	4.3	336	2	I49582	CD1.1 - mouse	1244	71.5	4.2	366	2	I38507	MHC class I histoc
1172	72	4.3	350	2	I54308	MHC HLA B71 - huma	1245	71.5	4.2	370	2	A39115	glucan endo-1,3-be
1173	72	4.3	354	2	S24437	class I histocompa	1246	71.5	4.2	380	2	E87729	protein Y23H5A.4 l
1174	72	4.3	362	2	S24435	class I histocompa	1247	71.5	4.2	398	1	S45545	GTP cyclonhydrolase
1175	72	4.3	362	2	S16789	class I histocompa	1248	71.5	4.2	398	2	H96967	protein containing
1176	72	4.3	365	2	I72170	MHC class I histoc	1249	71.5	4.2	426	2	T28563	hypothetical prote
1177	72	4.3	365	2	I38610	MHC class I histoc	1250	71.5	4.2	426	2	C36850	A2IR protein - var
1178	72	4.3	369	2	S12406	glucan endo-1,3-be	1251	71.5	4.2	428	1	AJRXOD	glutamate-ammonia
1179	72	4.3	386	2	A41950	retrovirus-related	1252	71.5	4.2	436	2	A53568	methylcrotonoyl-Co
1180	72	4.3	397	2	B87343	conserved hypochet	1253	71.5	4.2	468	2	B84540	acid phosphatase (
1181	72	4.3	406	2	B35878	class I major hist	1254	71.5	4.2	482	2	T47720	pyruvate kinase-11
1182	72	4.3	416	1	A42879	advanced glycoeyla	1255	71.5	4.2	497	2	E86485	hypothetical prote
1183	72	4.3	436	2	T16638	hypothetical prote	1256	71.5	4.2	528	2	PC4025	intercellular adhe
1184	72	4.3	450	1	MHDG	Ig mu chain C regi	1257	71.5	4.2	539	2	S16989	dihydroallopinamide
1185	72	4.3	450	1	MHDG	Ig mu chain C regi	1258	71.5	4.2	557	2	AF0274	ribulokinase (EC 2
1186	72	4.3	505	2	T33821	hypothetical prote	1259	71.5	4.2	586	2	T19075	hypothetical prote
1187	72	4.3	505	2	T07863	cellulase (EC 3.2.	1260	71.5	4.2	591	2	AB0509	oxalacetate decar
1188	72	4.3	520	2	A71564	hypothetical prote	1261	71.5	4.2	591	2	AB0509	transferring prote
1189	72	4.3	559	2	A36187	interleukin-1 rece	1262	71.5	4.2	640	1	A42908	meprin A (EC 3.4.2
1190	72	4.3	580	2	T28725	hypothetical prote	1263	71.5	4.2	668	1	A42908	pepa protein - Pse
1191	72	4.3	592	2	T43402	probable protein k	1264	71.5	4.2	687	2	T09051	hypothetical prote
1192	72	4.3	828	2	T22367	p-cadherin precurs	1265	71.5	4.2	702	2	E69498	cyclomalodextrin
1193	72	4.3	828	2	T22367	hypothetical prote	1266	71.5	4.2	704	2	I39805	hypothetical prote
1194	72	4.3	915	1	A49714	protein-tyrosine k	1267	71.5	4.2	710	2	B96540	hypothetical prote
1195	72	4.3	994	1	A32792	Ca2+-transporting	1268	71.5	4.2	747	2	B71417	cellulase (EC 3.2.
1196	72	4.3	997	1	PWRBSC	Ca2+-transporting	1269	71.5	4.2	747	2	B47093	transforming prote
1197	72	4.3	997	2	B31981	Ca2+-transporting	1270	71.5	4.2	761	1	TVHOMB	transforming prote

1271	71.5	4.2	811	2	PN0689	connectin 1 - chic
1272	71.5	4.2	825	2	A59296	alpha-L-arabinofur
1273	71.5	4.2	828	2	S52393	beta-galactosidase
1274	71.5	4.2	857	2	T04208	probable anthranil
1275	71.5	4.2	960	1	UN0677	protein-tyrosine k
1276	71.5	4.2	1137	2	B90734	probable host spec
1277	71.5	4.2	1138	2	D85584	probable tail comp
1278	71.5	4.2	1179	2	C36792	hypothetical prote
1279	71.5	4.2	1211	2	S68251	phospholipase C, i
1280	71.5	4.2	1236	2	JC7503	protein-tyrosine p
1281	71.5	4.2	1345	2	S55669	legume protein 7
1282	71.5	4.2	1441	2	A86685	prophage p11 prote
1283	71.5	4.2	1490	2	JC5145	DNA (cytosine-5-)-
1284	71.5	4.2	1612	2	AB1347	probable peptidogl
1285	71.5	4.2	1630	2	A53577	asacetic sialoglyco
1286	71.5	4.2	1815	2	B95942	conserved hypochet
1287	71.5	4.2	1939	2	D97316	probable S-layer p
1288	71.5	4.2	1946	2	AC2141	serine/threonine k
1289	71.5	4.2	3131	2	S39842	emulatin synthetas
1290	71.5	4.2	3191	2	T22945	hypothetical prote
1291	71	4.2	87	2	PH1082	Ig light chain V r
1292	71	4.2	98	2	S26911	Ig heavy chain V r
1293	71	4.2	115	1	KVMSL7	Ig kappa chain pre
1294	71	4.2	166	2	PL0012	Ig heavy chain pre
1295	71	4.2	180	2	G69222	molybdenum formylm
1296	71	4.2	254	2	S48547	probable membrane
1297	71	4.2	287	2	B69901	cell wall-binding
1298	71	4.2	321	2	AC0821	probable exported
1299	71	4.2	336	2	C27658	pregnancy-specific
1300	71	4.2	357	2	S09269	Ig alpha chain C r
1301	71	4.2	362	2	JH0541	class I histocompa
1302	71	4.2	362	2	JH0539	class I histocompa
1303	71	4.2	362	2	JH0540	class I histocompa
1304	71	4.2	362	2	I56149	lymphocyte antigen
1305	71	4.2	362	2	I84488	lymphocyte antigen
1306	71	4.2	362	2	I54505	lymphocyte antigen
1307	71	4.2	362	2	I54314	MHC HLA-B39N - hum
1308	71	4.2	362	2	I59645	HLA-B-6701 - human
1309	71	4.2	362	2	I54298	gene HLA-B protein
1310	71	4.2	362	2	I68850	MHC class I histoc
1311	71	4.2	364	2	D35997	MHC class I histoc
1312	71	4.2	367	1	MHCH	Ig mu chain C regi
1313	71	4.2	368	2	D90607	hypothetical prote
1314	71	4.2	374	2	F69233	carbamoyl-phosphat
1315	71	4.2	425	2	C64523	isocitrate dehydro
1316	71	4.2	427	2	T05019	hypothetical prote
1317	71	4.2	427	2	A11264	N-acetylmuramoyl-L
1318	71	4.2	453	2	H96798	hypothetical prote
1319	71	4.2	459	2	T43538	zinc finger protei
1320	71	4.2	476	2	A70318	aldehyde dehydroge
1321	71	4.2	481	2	JQ1147	N-acetylmuramoyl-L
1322	71	4.2	509	2	AC2217	hypothetical prote
1323	71	4.2	511	1	VGBEP4	glycoprotein C - h
1324	71	4.2	513	1	A48233	polyomavirus enhan
1325	71	4.2	520	2	G70597	probable proteinas
1326	71	4.2	526	2	S53871	Pmel 17 protein -
1327	71	4.2	656	2	D96831	hypothetical prote
1328	71	4.2	662	2	JC7906	sucrose 1F-fructos
1329	71	4.2	681	2	I53743	glutamine-fructose
1330	71	4.2	744	2	AF0410	GRP diaphosphokinas
1331	71	4.2	771	2	T13618	hypothetical prote
1332	71	4.2	776	2	B41704	genome polypeptid
1333	71	4.2	776	2	A41704	genome polypeptid
1334	71	4.2	796	2	A90541	hypothetical prote
1335	71	4.2	972	1	TVH0MD	macrophage colony-
1336	71	4.2	976	1	TVMSMD	macrophage colony-
1337	71	4.2	994	2	A48849	Ca2+-transporting
1338	71	4.2	994	2	A70776	Probable glnR - My
1339	71	4.2	1001	1	PWRBFC	Ca2+-transporting
1340	71	4.2	1067	2	T28663	hypothetical prote
1341	71	4.2	1135	2	JS0605	M polypeptid - Ha
1342	71	4.2	1142	2	GNVUPH	M polypeptid prec
1343	71	4.2	1157	2	P97255	fusion of alpha-gi

1344	71	4.2	1330	2	B70836	hypothetical prote
1345	71	4.2	1554	2	C72647	hypothetical prote
1346	71	4.2	1653	2	B91052	hypothetical prote
1347	71	4.2	1653	2	P85896	hypothetical prote
1348	71	4.2	2256	2	AD1018	large repetitive p
1349	71	4.2	4351	2	T00252	MEGF1 protein - ra
1350	70.5	4.2	98	2	PH1061	Ig light chain V r
1351	70.5	4.2	107	2	A26945	T-cell receptor de
1352	70.5	4.2	108	2	C10502	Ig kappa chain V r
1353	70.5	4.2	115	2	B26524	T-cell receptor be
1354	70.5	4.2	115	2	A30995	T-cell receptor be
1355	70.5	4.2	128	2	PN0445	Ig kappa chain pre
1356	70.5	4.2	137	2	S03477	T-cell receptor al
1357	70.5	4.2	142	2	A10577	conserved hypochet
1358	70.5	4.2	180	2	T18313	hypothetical prote
1359	70.5	4.2	225	2	AE2347	ribonuclease HII l
1360	70.5	4.2	228	2	S29575	Ig light chain - r
1361	70.5	4.2	235	2	S25754	Ig lambda chain -
1362	70.5	4.2	266	2	B82655	UDP-3-O-(R-3-hydro
1363	70.5	4.2	269	2	H84313	hypothetical prote
1364	70.5	4.2	272	2	C75560	conserved hypochet
1365	70.5	4.2	292	2	C84461	En/spm-like transp
1366	70.5	4.2	328	2	S65023	glucan endo-1,3-be
1367	70.5	4.2	340	2	A95939	probable spermidin
1368	70.5	4.2	345	2	F82528	hypothetical prote
1369	70.5	4.2	348	2	S09270	hypothetical prote
1370	70.5	4.2	355	2	B97795	Ig alpha chain C r
1371	70.5	4.2	372	2	T09962	peptide chain rele
1372	70.5	4.2	389	2	A44832	cyclin A-type - Ma
1373	70.5	4.2	397	2	S52783	aspartate estA - Ps
1374	70.5	4.2	406	2	D90492	hypothetical prote
1375	70.5	4.2	419	2	A36109	pregnancy-specific
1376	70.5	4.2	424	1	A36000	sperm-binding glyc
1377	70.5	4.2	445	2	A84410	hydroxymethylpyrim
1378	70.5	4.2	448	2	S65260	probable membrane
1379	70.5	4.2	456	2	C57742	cycloin II - maize
1380	70.5	4.2	482	2	JB0395	phospho-beta-galac
1381	70.5	4.2	483	2	E71681	isocitrate dehydro
1382	70.5	4.2	485	2	S36772	E-selectin - bovin
1383	70.5	4.2	520	2	S07375	flagellin H-1 - Sa
1384	70.5	4.2	520	2	A64033	hypothetical prote
1385	70.5	4.2	532	1	A28949	intercellular adhe
1386	70.5	4.2	539	2	JH0263	carboxy-terminal p
1387	70.5	4.2	555	2	T43847	DNA-directed RNA p
1388	70.5	4.2	577	2	A95902	probable glycerol-
1389	70.5	4.2	600	2	AH2623	60 kd inner-membra
1390	70.5	4.2	600	2	G97405	60K inner-membrane
1391	70.5	4.2	606	2	T13152	WDRI protein - hum
1392	70.5	4.2	612	2	AF0079	DNA polymerase sig
1393	70.5	4.2	629	2	A46500	Ly-9.2 antigen - m
1394	70.5	4.2	666	2	C90464	hypothetical prote
1395	70.5	4.2	682	2	T10319	envelope protein B
1396	70.5	4.2	727	2	D75122	hypothetical prote
1397	70.5	4.2	764	2	T39194	5-methyltetrahydro
1398	70.5	4.2	774	2	A39832	scarabous locus (ac
1399	70.5	4.2	782	2	AF0179	conserved hypochet
1400	70.5	4.2	787	2	A75347	GRP pyrophosphokin
1401	70.5	4.2	846	1	PNECA	penicillin amidase
1402	70.5	4.2	856	2	I58411	protein-tyrosine k
1403	70.5	4.2	878	2	E97302	hypothetical prote
1404	70.5	4.2	878	2	AD0664	probable exported
1405	70.5	4.2	879	2	S64755	hypothetical prote
1406	70.5	4.2	905	1	IJX1C1	N-cadherin 1 precu
1407	70.5	4.2	1043	2	F97302	hypothetical prote
1408	70.5	4.2	1133	1	A43964	M polypeptid prec
1409	70.5	4.2	1134	1	A43960	M polypeptid prec
1410	70.5	4.2	1134	1	GNVU22	M polypeptid prec
1411	70.5	4.2	1210	1	S35548	DNA-directed RNA p
1412	70.5	4.2	1603	1	VIRK5	vitellogenin vit-5
1413	70.5	4.2	1617	2	B86483	protein F5J5.15 (i
1414	70.5	4.2	1666	1	C3GP	complement C3 prec
1415	70.5	4.2	1804	2	A11850	serine/threonine k
1416	70.5	4.2	2037	2	T16881	hypothetical prote

hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
large repetitive p
MEGF1 protein - ra
Ig light chain V r
T-cell receptor de
Ig kappa chain V r
T-cell receptor be
T-cell receptor be
Ig kappa chain pre
T-cell receptor al
conserved hypochet
hypothetical prote
ribonuclease HII l
Ig light chain - r
Ig lambda chain -
UDP-3-O-(R-3-hydro
hypothetical prote
conserved hypochet
En/spm-like transp
glucan endo-1,3-be
probable spermidin
hypothetical prote
hypothetical prote
Ig alpha chain C r
peptide chain rele
cyclin A-type - Ma
aspartate estA - Ps
hypothetical prote
pregnancy-specific
sperm-binding glyc
hydroxymethylpyrim
probable membrane
cycloin II - maize
phospho-beta-galac
isocitrate dehydro
E-selectin - bovin
flagellin H-1 - Sa
hypothetical prote
intercellular adhe
carboxy-terminal p
DNA-directed RNA p
probable glycerol-
60 kd inner-membra
60K inner-membrane
WDRI protein - hum
DNA polymerase sig
Ly-9.2 antigen - m
hypothetical prote
envelope protein B
hypothetical prote
5-methyltetrahydro
scarabous locus (ac
conserved hypochet
GRP pyrophosphokin
penicillin amidase
protein-tyrosine k
hypothetical prote
probable exported
hypothetical prote
N-cadherin 1 precu
hypothetical prote
M polypeptid prec
M polypeptid prec
M polypeptid prec
DNA-directed RNA p
vitellogenin vit-5
protein F5J5.15 (i
complement C3 prec
serine/threonine k
hypothetical prote

[illegible]

DN-cadherin - fruit genome polyprotein
T-cell receptor de T-cell receptor al
Ig lambda chain pr Ig lambda chain pr
Ig kappa chain pr T cell receptor al
outer membrane pro T-cell receptor be
T-cell receptor al hypothetical prote
Ig lambda chain - hypothetical prote
glycoprotein G - b Fc gamma (IgG) rec
glycoprotein G - b MHC class I histoc
hypothetical prote hypothetical prote
hypothetical prote conserved hypocht
urate oxidase (EC dehydroxylat trans
deoxyribonuclease class I histocompa
class I histocompa MHC class I histoc
MHC class I histoc MHC class I histoc
MHC HLA-B18 chain MHC class I histoc
hypothetical prote hypothetical prote
hypothetical prote alcohol dehydrogen
conserved hypocht hypothetical prote
hypothetical prote probable esterase
large surface anti conserved hypocht
serine proteinase zinc-finger protei
rhamnulokinase (EC conserved hypocht
inulinase (EC 3.2. hypothetical prote
hypothetical prote involved in polyke
alpha-acetolactate intrileukin 1 recep
hypothetical prote ABC transporter, A
probable DNA ligase 6-methylsalicylic
dnak-type molecule hypothetical prote
beta-D-glucan exch probable GTP-bind
prolyl oligopeptid coat protein VP1 -
catalase HPII [amp catalase, hydrioper
hypothetical prote SCV1 protein - yea
hypothetical prote citin, muscle - ch
probable endopepti bryevian precursor
bryevian precursor hypothetical prote
translatation initia male-specific legh
hypothetical prote receptor-protein t
protein-cytrovine k regulatory factor

1490	70	4.1	988	2	T08102	myrosinase-binding
1491	70	4.1	1001	2	T00532	probable cadmium-t
1492	70	4.1	1016	2	T30943	aminopeptidase (EC
1493	70	4.1	1025	2	A83186	probable RND efflu
1494	70	4.1	1089	1	S33727	platelet-derived g
1495	70	4.1	1108	1	S45917	probable serine/th
1496	70	4.1	1133	2	E86308	hypothetical prote
1497	70	4.1	1172	2	F84572	probable cadmium-t
1498	70	4.1	1189	2	T17068	homeodomain-intera
1499	70	4.1	1402	2	D70634	probable polykerid
1500	70	4.1	1409	2	T42522	protein-tyrosine-p

ALIGNMENTS

RESULT 1

J:Functional_adhesion_molecule_precursor - human
 N:Alternate_names: P11_platelet_antigen; platelet_adhesion_molecule_PAM-1; platelet_P11
 C:Species: Homo sapiens (man)
 C:Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: A59406; S56749
 J:Okaki, H.; Ishii, K.; Horizuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.;
 J:Immunol. 163, 553-557, 1999
 A:Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut
 A:Reference_number: A59406; MUID:99325940; PMID:1035639
 A:Accession: A59406
 A:Status: preliminary
 A:Molecule_type: DNA
 A:Residues: 1-299 (102A>)
 A:Cross-references: UNIPROT:Q9Y624; GB:AAD42050; NID:95326797; P1DN:AAD42050.1
 R:Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
 Biochem. J. 310, 155-162, 1995
 A:Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of
 A:Reference_number: S56749; MUID:95374438; PMID:7646439
 A:Accession: S56749
 A:Molecule_type: Protein
 A:Residues: 28-49, 'X', 51-53, 62-73, 'E', 75-103, 123, 'F', 125-130; 'FDKDXITLYLNXY', 'LT', 206, 'X'
 A:Note: the order of the peptides other than the amino terminus was not determined
 C:Genetics:
 A:Gene: JAM
 C:Keywords: glycoprotein; phosphoprotein; platelet_aggregation; platelet_membrane
 F,1-25;Domain: signal_sequence #status_predicted <Sig>
 J,26-239;Product: junctional_adhesion_molecule #status_predicted <MnT>

Query Mat

Query March	10.6%	Score 178.5;	DB 2;	Length 299;
Best Local Similarity	26.5%	Pred. No. 2.3e-06;		
Matches 65; Conservative	36;	Mismatches 93;	Indels 51;	Gaps 11

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QY      1 MGILLGLLLGLLGLLVTDTYGRPLLEVPBSVTGPMKGDVNLPTCTYDPLQGYQVLYKMLVQR 60
Dh      17 LAILLCSLALSGSVTHS--SEPEVRIRPEN-----NPVYLSGAY---GGFSSPREW----- 62
QY      61 GSDPVTITFRDSSGDHIOAQYQGRFLHVSHK-----VPGDVSLOLSTLEMDKDSHYTCFV 115
Dh      63 -----KFDGGPTTRLVCTNNKMTITSYEDRVTFPLPTGTIGFSSVRE--DTGYTCMV 111
QY      116 TWOTPDGNOVBRDKITELRVOKLSYKSKPLVTGSGGYTFVQGRISLOCOAR--GSPPIIS 174
Dh      112 SEEGGNSYGEVAVKLIIVL---VPPSKTVAIPIS---SATIGRAVVLITGEOGDSFPSE 164
QY      175 YIWKY-----QQTN-----NOEPIKAVATLSTLLFKPRAVIADSGSYFCTAKQGVGSEOH 222
Dh      164 YTMFKDGLVMPFNPNSTRAFSSSVLANPTTGELVDPDLASDITGEXSCEARNGYGTPTMT 223
QY      223 SDIYK 227
Dh      224 SNAVR 228

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RESULT 2
I38346

elastic titin - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I38346
R/Labett, S.; Kojmer, B.
Science 270, 293-296, 1995
A/Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A/Reference number: A57430; MUID:96026330; PMID:7569978
A/Accession: I38346
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 17962 <RBS>
A/Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101
C/Genetics:
A/Genes: GDB:TTN
A/Cross-references: GDB:127867; OMIM:188840
A/Map position: 2q31-2q31

Query Match 10.2%; Score 172; DB 2; Length 7962;
Best Local Similarity 27.5%; Pred. No. 0.00045;
Matches 67; Conservative 30; Mismatches 85; Indels 62; Gaps 11;

QY 16 DTGRRPILVPEPES-VYGPWKGDVNL-----CTYDPLQGYOVLVK-----LYORSGDP 64
DB 860 DSSGALIVQEPSPVTPKPSKDV-LPGSAVCLKSTPQSGSTPLTRFKGNKELVSGSCY 918
QY 65 VTFILNDSGSDHIQQAQYQGRLVHSHKVPQGVLSQLSTLEMDRSHYTCVETWQTPDG-- 122
DB 919 IT-----KEALSSLELYLVTSISGTYTCV--NVAGV 953
QY 123 ---NOVVRDKITELRVOKLSVSKPTVTTSYGFTVPQGRISLQCGARSPISYIWK 179
DB 954 CSANLFFKEPAT--PVEKLEPSQ-----LTKKGATQLACKVGTGPPIKITWFA 1000
QY 180 QQNNQEPK-----VATLSTLFFKRAVINDSGSYFACQVSGEHSNIVFVYKDS 234
DB 1001 NDRIRIKSSKRRMSFVSTAVLRLTVGIDSGIMCEAQNAGSDHCSSIV--IVKSP 1058
QY 235 KLLK 238
DB 1059 YFVK 1062

RESULT 3
JC7780
C/Species: Bos primigenius taurus (cattle)
C/Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C/Accession: JC7780
R/Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A/Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recept
A/Reference number: JC7780
A/Contents: liver
A/Accession: JC7780
A/Molecule type: mRNA
A/Residues: 1-365 <THO>
A/Cross-references: UNIPROT:Q8MWV3; GB:A033651
C/Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 10.0%; Score 169; DB 2; Length 365;
Best Local Similarity 24.8%; Pred. No. 1.6e-05;
Matches 85; Conservative 40; Mismatches 120; Indels 98; Gaps 17;

QY 1 MGILLGLLGHITVDPYGRPILEVPESVTPKGP-VNLPCTY-----DPLQGYQV 52
DB 1 MEHLRFLLCGVADTRGLST-TTPQMEKAKGETAVLPCKFTLGPEDQGLD----- 54
QY 53 LVKMLVORGS---DPTTFLNDSGSDHIQQAQYQ--GRIVSHK--VPGVLSQLSTL 103
DB 55 -IEMILSPADNQNVDVYIY---SGDKIYDYYQDLKGRVHFTSDNLSGDSASINVTML 110
QY 104 EMDRSHYTCVETWQTPDGQNVVRDKITELRVOKLSVSKPTVTTSYGFTVPQ-----GM 159

Db 111 QLSDITGYCKYKAPGVNKK-----KIQLTVLVK-----SGIRCYDGSSEIGN 156
QY 160 RSLSQCAR-GSPISYIWKQNTNQP---IKVATLSTLFFKRAVINDSGSYFCTAG 215
DB 157 DFKLKEPESGLPLEYEQKLSDSQKLPTSMLEPENTSVISVKNASAYSGTYTIVN 216
QY 216 QVSGEHSNDIVFVVDSSKLTKEAPETWTYPLKATSVKQSWDWTMDMGVIGETS 275
DB 217 RVGSDQ-----CLRLDVPPSNR-----AGTI 239
QY 276 AGRGSLPFAIILISLCCMVFTWYMYMLCRKTSQGEHYE 318
DB 240 AG-----AVIGTLALVIALIYF-----CCHKRRREKYE 270

RESULT 4
B49120
C/Species: Drosophila melanogaster
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C/Accession: B49120; S18010
R/Shihido, E.; Higashijima, S.; Emori, Y.; Saigo, K.
Development 117, 751-761, 1993
A/Title: Two FGF-receptor homologues of Drosophila: one is expressed in mesodermal prim
A/Reference number: A49120; MUID:93321617; PMID:8330538
A/Accession: B49120
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-1052 <SHI>
A/Cross-references: UNIPROT:Q09147; GB:X74031; GB:S63797; NID:g397600; PIDN:CAA52190.1;
A/Experimental source: pupa
A/Note: sequence extracted from NCBI backbone (NCBIN:135151, NCBI:135153)
R/Shihido, E.; Emori, Y.; Saigo, K.
FEBS Lett. 289, 235-238, 1991
A/Title: Identification of seven novel protein-tyrosine kinase genes of Drosophila by th
A/Reference number: S17552; MUID:92008631; PMID:1915852
A/Accession: S18010
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 869-922 <SH2>
C/Genetics:
A/Genes: FlyBase:bc1; dtk2
A/Cross-references: FlyBase:FBgn0005592
C/Superfamily: protein kinase homology
C/Keywords: ATP; growth factor receptor; phosphotransferase; tyrosine-specific protein k
F:118-126/Domain: protein kinase homology <KIN>
F:118-126/Region: protein kinase ATP-binding motif

Query Match 8.5%; Score 143.5; DB 2; Length 1052;
Best Local Similarity 23.4%; Pred. No. 0.0055;
Matches 71; Conservative 44; Mismatches 119; Indels 69; Gaps 14;

QY 16 DTGRRPILVPEPESVTPKGDVNLPCT-YDP-LOGTYOVLVKLVORSGDP 64
DB 130 DLFPPLNRSRLKLLQLPLKPTORTAGLPQLNCSPPMDPAKG--VNISWL----- 179
QY 65 VTFILNDSGSDHIQQAQYQGRLVHSHKVPQGVLSQLSTLEMDRSHYTCVETWQTPDG 124
DB 180 -----HIDPQILAGGRIRLK--RSLVVGQLQPDADASYCELVE-----OD 221
QY 125 VVRDKITELRVOKLSVSKPTVTTSYGFTVPQGRISLQCGARSPISYIWKQ 181
DB 222 CQRNMPQLEVISRKHVYPMLEKGVPRNTSIALGNVSIIECLLEDSALEPKITWL-HKGN 280
QY 182 TNN-----QEPKATLSTLFFKPAVI-----ADSSYFCTAGQVSGE 222
DB 281 ADNIDDLQRLREGSQLPVDVTRLITRMDPQVLLGNVLMDGGWYICIAENQGRVA 340
QY 223 SDIVFVVDSSKLTKEAPETWTYPLKATSVKQSWDWTMDMGVIGETSAGRSKL 282
DB 341 ASYVDLSPSPSDTTTYVRIIT--TTIVASPIPTASTGEDND--DVENPAADSGGVGP-- 393

QY 283 PVF 285
DB 394 PVF 396

RESULT 5

SI8252
heparan sulfate proteoglycan - mouse
N/Alternate names: perlecan
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 12-Jul-2004
R/Accession: SI8252; A31917; S66460
R/Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, B.; Sasaki, M.; Yamada, Y.; He
J. Biol. Chem. 266, 22939-22947, 1991
A/Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly
adhesion molecule.
A/Reference number: SI8252; MUID:92078153; PMID:1744087
A/Accession: SI8252
A/Molecule type: mRNA
A/Residues: 1-3707 <NO>
A/Cross-references: UNIPROT:Q05793; EMBL:M7174; NID:g200295; PIDN:AAA3991.1; PID:g2002
R/Noonan, D.M.; Horigan, B.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hase
J. Biol. Chem. 263, 16379-16387, 1988
A/Title: Identification of cDNA clones encoding different domains of the basement membra
A/Reference number: A92680; MUID:89034110; PMID:2972708
A/Accession: A31917
A/Molecule type: mRNA
A/Residues: 940-1601 <NO2>
A/Cross-references: GB:U04054; NID:g200252; PIDN:AAA3989.1; PID:g200253
A/Accession: B31917
A/Molecule type: mRNA
A/Residues: 1870-2600 <NO3>
A/Cross-references: GB:U04055; NID:g200300; PIDN:AAA3991.1; PID:g200301
R/Schulze, B.; Mann, K.; Ballestrut, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A/Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A/Reference number: S66460; MUID:95377282; PMID:7649154
A/Accession: S66460
A/Molecule type: protein
A/Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>
C/Keywords: glycoprotein
F/159-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F/325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F/368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F/764-811/Domain: laminin-type EGF-like homology <LEG>
F/1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F/1563-1610/Domain: laminin-type EGF-like homology <LEG8>
F/1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F/3163-3198/Domain: EGF homology <EGF>
F/3370-3423/Domain: laminin G repeat homology <EGF>
F/3464-3492/Domain: EGF homology <EGF>
F/1556, 1891, 2336, 2394, 2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 139.5; DB 2; Length 3707;
Best Local Similarity 25.1%; Pred. No. 0.055;
Matches 66; Conservative 31; Mismatches 105; Indels 61; Gaps 14;
QY 13 LTVDVT---VGRPLFVBSVTPGPKGDVNLPTCTYDPLQGYTVLVKMLVQRSGDPVTFIF 68
DB 2521 LIYDTGVAPCTPOVQVBS-----ELTLEA-----GHTATL--HCSATGNPPT-- 2563
QY 69 LRDSGGHIQOAKYQGRHLVSHKVPQDVSLSTLEMDRSHYCEVTWQTTPDGNQVVRD 128
DB 2564 -----IHWSKLRAPLPMQHRLEGNTLIVIPVAAQDSQGYICNAT-----NSAGHT 2608
QY 129 KITELAVQKLSVSKPTVTGSGVGFVPO-----GMRISQCARSGSPISYIWKQOT 182
DB 2609 EATV---LHVESPP-----YATIPERTSAQPNLVQOCLAHGTPPLTYM--SLV 2656
QY 183 NNQPIKAVATLSTLL-FKPAVIADSGSYCTAKGVSGEHSQSDIVKFPVQSSKILTKTKT 241
DB 2657 GGVLPEKAVVAVNQLRLREPTVPEDSGRYRCQVSNRVSAAE--AFAYQLVQSSSNLPDTS 2714

QY 242 ----EATTTTPKATSTYKOS 260
DB 2715 IPGSGTPTVQVTPQLETRNIGAS 2737

RESULT 6

PN0568
connectin 3B - chicken (fragment)
N/Alternate names: Cn3B protein
C/Species: Gallus gallus (chicken)
C/Date: 03-May-1994 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
R/Accession: PN0568
R/Maruyama, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanazawa, N.; Nakauchi, Y.; Kimura, S.
Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993
A/Title: A novel domain sequence of connectin localized at the 1 band of skeletal muscl
A/Reference number: PN0568; MUID:93356802; PMID:8352787
A/Accession: PN0568
A/Molecule type: mRNA
A/Residues: 1-1323 <MAR>
A/Cross-references: UNIPROT:Q08476; DDBJ:D16541; NID:g391629; PID:dl004495; PID:g391630
A/Experimental source: skeletal muscle
C/Comment: This protein string-like single molecule spans from the 2 line to the M line

Query Match 8.2%; Score 138.5; DB 2; Length 1323;
Best Local Similarity 21.4%; Pred. No. 0.018;
Matches 61; Conservative 38; Mismatches 117; Indels 69; Gaps 10;

QY 22 ILFVPSV---TGPMKGDVNLPTCTYDPLQGYTVLVKMLVQRSGDPVTFIFLRDSSGDHIQ 78
DB 143 ILRIPNKLKDQOYSGHINDSGDNCHAIILLEPPYVTFLEPVPQVTVGSASLQCC 202
QY 79 QAK-----YQ-----RLVSHKVPQDVSLQSTLBMDRSHYTCVTVQTP 120
DB 203 VAGTPREIVSWYKDTLRGTATVKNHFKNQV--ATLVFSQVDSDSGEYIKVENTVG 259
QY 121 DGNQ-----VVRKITELRQKLSVSKPTVTGSGVFTVPGMRISLQCARSGPISY 175
DB 260 EATSSSLITVQERLRLPSPFRKLRDVEIV-----GLVTFPGIAGSEPIEV 307
QY 176 IWKQQTNNQPIKIVAT--LSTLLFKPAVIAD---GSYPTAKGVSGEHSQSDIVKVV 230
DB 308 SWPRDNVAVEDNVHVSFDVNAIQLITLDSLSMGQYCTHSMIGT-----A 357
QY 231 KDSSKILKITEAPTTWTFPLKATSTYKOSWMTTMDGYLGETS 275
DB 358 SSSGKLVLTGKTPPFDPTRI-----TPVDGIIGESA 389

RESULT 7

T42633
connectin/titin - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
R/Accession: T42633
R/Iejima, H.; Ohnaka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; M
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A/Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin r
A/Reference number: Z22221; MUID:96254045; PMID:8660363
A/Accession: T42633
A/Status: preliminary; translated from GB/EMBL/DDB
A/Molecule type: mRNA
A/Residues: 1-4162 <YAJ>
A/Cross-references: UNIPROT:Q98918; EMBL:D83390; NID:g1513029; PIDN:BA11908.1; PID:g15
A/Experimental source: breast muscle
C/Keywords: skeletal muscle

Query Match 8.2%; Score 138.5; DB 2; Length 4162;
Best Local Similarity 21.4%; Pred. No. 0.076;
Matches 61; Conservative 38; Mismatches 117; Indels 69; Gaps 10;
QY 22 ILFVPSV---TGPMKGDVNLPTCTYDPLQGYTVLVKMLVQRSGDPVTFIFLRDSSGDHIQ 78

Db 3895 ILBIPNSKLEDDQGSCHINENDSGDNCAGATILBEPYFVTPLEPVQVTDGSAISLQCG 3954
 QY 79 QAK-----YGG-----RLVSHKVPGDVSLQSTLEMDRSHYTCBETWQTP 120
 Db 3955 VAGTPEMVSWYGDGTGRTATVKNHFKQV---ALVVSQVSDSGSEYICKVENTWG 4011
 QY 121 DGNQ-----VVRDKITELRVQKLSVSKPVTVTGSGYFTVPOGMRISLQCGARSPISY 175
 Db 4012 EATSSSLTLVQGERKLPPSPFRKLRDHYETV-----GLPVPFDGNGISSEPIEV 4059
 QY 176 IWKQQTNNQEPKIVAT--LSTLFRKAVIADSGSYCTAKGVGSEHSDIYKVV 230
 Db 4060 SWKEDNVRVKEEDVNVHFSFDNVAIIQILTKDLSLMOQYCTASNAIGT-----A 4109
 QY 231 KDSKLLKTKTEAPTMTVTPKATSTVKGSMWTDMDGYLGENTS 275
 Db 4110 SSSGKLVLEGGKTPPPFDTPF-----TPVDGILIGESA 4141

RESULT 8

T08678

hypothetical protein DKFZp56411922.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08678

R/Wambolt, R.; Heubner, D.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16469

A/Accession: T08678

A/Molecule type: mRNA

A/Residues: 1-584 <MAN>

A/Cross-references: UNIPROT:Q9Y3Y8; EMBL:AL049946

A/Experimental source: fetal brain; clone DKFZp56411922

C/Genetics:

A/Note: DKFZp56411922.1

Query Match 8.1%; Score 136; DB 2; Length 584;

Best Local Similarity 22.4%; Pred. No. 0.0099;

Matches 53; Conservative 37; Mismatches 99; Indels 48; Gaps 8;

QY 35 GDNVNECTYDPLQGYQVLYKLVQKSGDVTFLANDSGSDHICQAKYQGRHVSHPG 94
 Db 15 GDLKVCV--ATGLPPEISWLSLPDGLSNVMSQSDSGRKYR-----YVFN 61
 QY 95 DVSILSTLEMDRSHYTCBETWQTPDGNQVNRDKITELRVQKLSVSKP--TVTTGSGYR 153
 Db 62 NGTLVNEVGMREGEYTCFAE-----NOVGKD--EMRVKVVTAPTTINKTCLAV 112
 QY 154 TVPQGRISLQCGARSPISYIYW---KQNTNQEPIKAVTLSTLFRKAVIADSGSY 209
 Db 113 QVEYGVNVTVACBAKGEPMKVTWLSPTNKVIPTSSEKVIYQDGTLLIQAKRSDSGNV 172
 QY 210 FCTAKQVGEQH-----SDIVKPVKQSSKLLKTKTA--PT 245
 Db 173 TCLVRNSAGSDRTWIHVNVPKINGNPNPITTVAREIAAGSRKLDCKAGIPT 229

RESULT 9

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T20992; T24733

R/Sulston, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z19355

A/Accession: T20992

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5175 <WII>

A/Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:PI

A/Experimental source: clone F15G9

R/Kerhaw, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z19929

A/Accession: T24733

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5175 <W12>

A/Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A/Experimental source: clone T0989

C/Genetics:

A/Gene: CESP:F15G9.4a

A/Map position: X

A/Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;

; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;

1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1;

Query Match 7.9%; Score 133.5; DB 2; Length 5175;

Best Local Similarity 22.9%; Pred. No. 0.24;

Matches 48; Conservative 36; Mismatches 93; Indels 33; Gaps 6;

QY 76 HIQAKYQGRHVSHPGDVSLQSTLEMDRSHYTCBETWQTPDGNQVNRDKITELRV 135
 Db 2796 HAHDESQNGVITTSKTAANEKTLNVTNIQDDDEGFTYC-----TAVNEAGITKKPFLV 2850
 QY 136 -----QKLSVSKPVTVTGSGYFTVPOGMRISLQCGARSPISYIWKQQTNNQ 186
 Db 2851 IETPYFLDQOKL-----YPIILGRLTLDCAATGTPPTILFMKDGRLNE 2896
 QY 187 PIKVAATL-STLFRKAVIADSGSYCTAKGVGSEHSDIYKVV--KQSSKLLKTKTA 243
 Db 2897 SDEVDIIGTLVINDPQKEBGRYTCIAENKGRSEKDMVAVLLPPLKSKWINVEVQA 2956
 QY 244 --PTMTVTPKATSTVKGSMWTDMDGYL 271
 Db 2957 GBDPLTECFIEDTSGVHTMSRQFGKDGQL 2986

RESULT 10

T43290

hemiscentin precursor - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T43290; T20993; T24734

R/Vogel, B.E.; Hedgecock, E.M.

submitted to the EMBL Data Library, June 1998

A/Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ-

R/Sulston, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z22396

A/Accession: T43290

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-5198 <VOG>

A/Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1

A/Experimental source: clone F15G9

A/Reference number: Z19355

A/Accession: T20993

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5198 <WII>

A/Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

A/Experimental source: clone F15G9

R/Kerhaw, J.

submitted to the EMBL Data Library, December 1994

A/Reference number: Z19929

A/Accession: T24734

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-5198 <W12>

A/Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b

A/Experimental source: clone T0989

C/Genetics:

A/Gene: him-4; F15G9.4b

A/Map position: X

A/Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;


```

: 2512/2: 2593/3: 2759/1: 2852/1: 2889/3: 2913/3: 2941/1: 2967/3: 2991/3: 3033/1
: 4425/1, 4361/1, 4408/1, 4456/1, 4480/1, 4647/3, 4838/1, 4902/1, 4964/1, 5034/1, 5100/
Query Match 7.9%; Score 133.5; DB 2; Length 5198;
Best Local Similarity 22.9%; Pred. No. 0.24;
Matches 48; Conservative 36; Mismatches 93; Indels 33; Gaps 6;

Qy 76 HIOQAKYQGRHSHKPGVNSLQSLTLEMDRSHYTCVWQRPDGNQVDRDITLRY 135
Db 2796 HAHDESVQNGVITSKYANEXTLAVNTNIQLDDEGFYC-----TAVNAGITKFFKLIV 2850
Qy 136 -----OKLSVSKPTVTGSGYGFVPOGMKRSIQCOARGSPISYIWKQQTNNQ 186
Db 2851 IETPFYFDQKL-----YPIIGKRLTLDCAATGTPPPIILFMKQKRLNE 2896
Qy 187 PIKAVTL-STLLFKPAVIADSGSYCTAKQGVSGEHSIDYKPVV--KDSGKLKRTKEA 243
Db 2897 SDEVDIIGSTLVINDPKQEVGRYTCIAENKAGSEKDMVVEVLLPRLSKEMINVEVQA 2956
Qy 244 --PTTMYPLKATSTYKQSDMTDMDGYL 271
Db 2957 GDPULTLEPIEDTSVGHITWSRQFGKQGL 2986

RESULT 11
PHEUGB
Platelet-derived growth factor receptor beta precursor - human
N:Containing: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C:Accession: A28206; A31195; A38268; A31925; B31925; C31925
R:Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3433-3439, 1988
A>Title: Cloning and expression of a cDNA coding for the human platelet-derived growth f
A:Reference number: A28206; MUID:8821915; PMID:2835772
A:Accession: A28206
A:Molecule type: mRNA
A:Residues: 1-1106 <GRO>
A:Cross-references: UNIPROT:P09619; GB:J03278; NID:G189731; PID:AAA60049.1; PID:G189732
R:Claesson-Welsh, L.; Eriksson, A.; Molen, A.; Severingsson, L.; Ek, B.; Oestman, A.; Bet
Mol. Cell. Biol. 8, 3476-3486, 1988
A>Title: cDNA cloning and expression of a human platelet-derived growth factor (PDGF) re
A:Reference number: A31195; MUID:8909694; PMID:2850496
A:Accession: A31195
A:Molecule type: mRNA
A:Residues: 1-240; 'D', 242-1106 <CLA>
A:Cross-references: GB:M21616; NID:G189729; PID:AAA36427.1; PID:G189730
R:Partanen, J.; Mekkela, T.P.; Altalo, R.; Lehtoelaho, H.; Altalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A:Reference number: A38268; MUID:91062389; PMID:2247464
A:Accession: A38268
A:Molecule type: nucleic acid sequence not shown
A:Residues: 828-884 <PAR>
R:Roberts, W.M.; Lock, A.T.; Rouseel, M.F.; Sherr, C.J.
Cell 55, 655-661, 1988
A>Title: Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.
A:Reference number: A90908; MUID:89028677; PMID:2846185
A:Accession: A31925
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 676-727 <ROB>
A:Accession: B31925
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 901-932 <RO2>
A:Accession: C31925
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1047-1106 <RO3>
C:Comment: The extracellular domain is predicted to include five immunoglobulin-like dom
C:Genetics:

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A:Gene: GDB:PDGFRB
A:Cross-references: GDB:120710; OMIM:173410
A:Map position: 5q31.5q32
A:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology
C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer
F:1.32/DNA: signal sequence #status predicted <Sig>
F:3.3-1106/Product: platelet-derived growth factor receptor beta #status predicted <MNT>
F:3.3-531/DNA: extracellular #status predicted <EXT>
F:4.7-102/DNA: immunoglobulin homology <IMM1>
F:142-192/DNA: immunoglobulin homology <IMM2>
F:228-293/DNA: immunoglobulin homology <IMM3>
F:429-510/DNA: immunoglobulin homology <IMM4>
F:532-555/DNA: transmembrane #status predicted <TM>
F:556-1106/DNA: intracellular #status predicted <INT>
F:558-965/DNA: protein kinase homology <KIN>
F:606-614/Region: protein kinase ATP-binding motif
F:45-89,103,215,230,292,307,354,371,468,479/Binding site: carbohydrate (Asn) (covalent)
F:54-100,149-190,235-291,436-508/Disulfide bonds: #status predicted
F:634/Active site: Lys #status predicted
F:857/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict

Query Match 7.9%; Score 133; DB 1; Length 1106;
Best Local Similarity 21.4%; Pred. No. 0.038;
Matches 60; Conservative 41; Mismatches 92; Indels 88; Gaps 11;

Qy 23 LEVDESITGPW-----KGVNLPCTYDPLQGYOVVYKMLVQSGSDPVTFLRDSG 74
Db 145 ITTPCRVTQDLVTLTKERGDVALPVPYHQKSGSI----- 182
Qy 75 DHIOAKYQGRHSHKPGVNSLQSLTLEMDRSHYTCVWQRPDGNQVDRDITLRY 134
Db 183 -----FEBRSYIKCTTID-----REVSDAYV-----VYRLQ 210
Qy 135 VQKLSVSKPTVTGSGYGFVPOGMKRSIQCOARGSPISYIWKQQTNNQ--EPKVA 191
Db 211 VSSINVSVAVQV-----VROGENTLMCIYIGNEVVAFEWTPYRKESGRVPEYTD 264
Qy 192 TL-----STLFPKPAVIADSGSYCTAKQGVSGEHSIDYKPVVYKQSDMTDMDGYL 244
Db 265 LIDMPYHRIKILHPSLELSDSGTYTCNVTSVNDHDEKALNTVVEG--YVRLAGEVG 323
Qy 245 TTTMYPLKATSTYKQSDMTDMDGYL 277
Db 324 TLQPAELHRSRTIQVPEAFPPVLMFKD--NRTLDGSSAG 363

RESULT 12
cell adhesion molecule apCAM (clone d12) - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004
C:Accession: C42632
R:Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A>Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastici
A:Reference number: A42632; MUID:92263095; PMID:1585176
A:Accession: C42632
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-765 <MAY>
A:Cross-references: UNIPROT:Q9TMA4
A:Experimental source: CNS
A>Note: sequence extracted from NCBI backbone (NCBI:101351)
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm

Query Match 7.8%; Score 132.5; DB 2; Length 765;
Best Local Similarity 20.7%; Pred. No. 0.026;
Matches 54; Conservative 31; Mismatches 63; Indels 113; Gaps 10;

Qy 104 EMDRSHYTCV-----TWQPDGNQVDRDITLRYVQKLSVSKPT-----VTTGSG 150
Db 230 KQGVKAVTQACGVPPVYQFKKGDVMTDEVNNGVLTINPLKTTDQATYTCIATNKG 289

```

QY 151 YGFT-----VP-----QGMRLSLOQARGSPPISTYI----- 177
|||
|||
Db 290 -GFAESSNTLDVAVPPPTIEDMEETDYAVSGOELITCTAGDPEPSYIMKKDGPQASATD 348
QY 178 -----YKQNTNOEPKIVATLST-LLFKPAVADSGSYFCTAKQGVSEQSHDIYK 228
|||
|||
Db 349 GIVNKGPTVEKVSNDMEKTVAQHMTFKPVTYQDAGTYICTASLVGSANKT--VKL 406
QY 229 VVK-----DSSKLTKTKT 241
|||
|||
Db 407 TVQYKPNFDTDFKEREFFGMRGHKANLTCQANANPVATIEWMPDAENPDDYSKAVRIPN 466
QY 242 EAPTTMTYPLKATSTYKQSWD 262
|||
|||
Db 467 EAPYTI-----NMLQKWD 479

RESULT 13

cell adhesion molecule apCAM (clone d15) - California sea hare
C/Species: Aplysia californica (California sea hare)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B42632
R/Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A/Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A/Reference number: A42632; PMID:92263095; PMID:1585176
A/Accession: B42632
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-812 <MAY>
A/Cross-references: UNIPROT:Q9TWA5
A/Experimental source: CNS
A/Note: sequence extracted from NCBI backbone (NCBIP:101346)
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match 7.8%; Score 132.5; DB 2; Length 812;
Best Local Similarity 20.7%; Pred. No. 0.028;
Matches 54; Conservative 31; Mismatches 63; Indels 113; Gaps 10;
QY 104 EMDRSHYTCV-----TWQTPDGNQVVRDKITELRVQKLSVSKPT-----VTTGSG 150
|||
|||
Db 230 KVGDEVKITCQATGVPPPTQFKKGDVMTDEMVGVLINPLKTTDQATYTCIATNKG 289
QY 151 YGFT-----VP-----QGMRLSLOQARGSPPISTYI----- 177
|||
|||
Db 290 -GFAESSNTLDVAVPPPTIEDMEETDYAVSGOELITCTAGDPEPSYIMKKDGPQASATD 348
QY 178 -----YKQNTNOEPKIVATLST-LLFKPAVADSGSYFCTAKQGVSEQSHDIYK 228
|||
|||
Db 349 GIVNKGPTVEKVSNDMEKTVAQHMTFKPVTYQDAGTYICTASLVGSANKT--VKL 406
QY 229 VVK-----DSSKLTKTKT 241
|||
|||
Db 407 TVQYKPNFDTDFKEREFFGMRGHKANLTCQANANPVATIEWMPDAENPDDYSKAVRIPN 466
QY 242 EAPTTMTYPLKATSTYKQSWD 262
|||
|||
Db 467 EAPYTI-----NMLQKWD 479

RESULT 14
A42632
cell adhesion molecule apCAM (clone d19) - California sea hare
C/Species: Aplysia californica (California sea hare)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A42632
R/Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A/Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A/Reference number: A42632; PMID:92263095; PMID:1585176
A/Accession: A42632
A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid
A/Residues: 1-932 <MAY>
A/Cross-references: UNIPROT:Q9TWA6
A/Experimental source: CNS
A/Note: sequence extracted from NCBI backbone (NCBIP:101342)
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match 7.8%; Score 132.5; DB 2; Length 932;
Best Local Similarity 20.7%; Pred. No. 0.033;
Matches 54; Conservative 31; Mismatches 63; Indels 113; Gaps 10;
QY 104 EMDRSHYTCV-----TWQTPDGNQVVRDKITELRVQKLSVSKPT-----VTTGSG 150
|||
|||
Db 230 KVGDEVKITCQATGVPPPTQFKKGDVMTDEMVGVLINPLKTTDQATYTCIATNKG 289
QY 151 YGFT-----VP-----QGMRLSLOQARGSPPISTYI----- 177
|||
|||
Db 290 -GFAESSNTLDVAVPPPTIEDMEETDYAVSGOELITCTAGDPEPSYIMKKDGPQASATD 348
QY 178 -----YKQNTNOEPKIVATLST-LLFKPAVADSGSYFCTAKQGVSEQSHDIYK 228
|||
|||
Db 349 GIVNKGPTVEKVSNDMEKTVAQHMTFKPVTYQDAGTYICTASLVGSANKT--VKL 406
QY 229 VVK-----DSSKLTKTKT 241
|||
|||
Db 407 TVQYKPNFDTDFKEREFFGMRGHKANLTCQANANPVATIEWMPDAENPDDYSKAVRIPN 466
QY 242 EAPTTMTYPLKATSTYKQSWD 262
|||
|||
Db 467 EAPYTI-----NMLQKWD 479

RESULT 15

S26180
neurofascin - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S26180
R/Volkmer, H.; Hasel, B.; Wolff, J.M.; Frank, R.; Reithen, F.G.
J. Cell Biol. 118, 149-161, 1992
A/Title: Structure of the axonal surface recognition molecule neurofascin and its relat
A/Reference number: S26180; PMID:92317154; PMID:1377696
A/Accession: S26180
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1272 <VOL>
A/Cross-references: UNIPROT:Q42414; EMBL:X65224; NID:G63659; PTDN:CAA46330.1; PID:G6366C
C/Superfamily: neural cell adhesion molecule I1; fibronectin type III repeat homology; 1
F/279-336/Domain: immunoglobulin homology <IMM>

Query Match 7.8%; Score 132.5; DB 2; Length 1272;
Best Local Similarity 22.2%; Pred. No. 0.049;
Matches 51; Conservative 38; Mismatches 88; Indels 53; Gaps 7;
QY 22 ILEVESYVPGKGDVNLPCYDPLQGYQVVKMLVGRGSDPVITFLRDSGDHIQAK 81
|||
|||
Db 150 VIEVDG-----APLSIQCNPP-----GLPPVIFWSSMSBPIHQK 188
QY 82 -----YQGLHVSXKVPDGVSLQLS-----TLEMDRSHYTCVYTWQTPDGNQVVRDK 129
|||
|||
Db 189 RVSGQNGDLYFSNWLQDAQTDYSCNARFHFTHITQCKNPYTLKTKKPKNNETSLRNH 248
QY 130 ITELRVQKLSVSKPT--VTTGSGYPTVQGMRLSLOQARGSPPISTYIMYK----- 179
|||
|||
Db 249 TMTYSARGVETTPSPMRYGTSSQOMVLRGVDLLCTASVAPADIMYKKGGLPAG 308
QY 180 --QNTNOEPKIVATLSTLLFKPAVADSGSYFCTAKQGVSEQSHDIYK 227
|||
|||
Db 309 KTKLENPKNALISNVSE-----EDSGEYFCIASNMGSIIRHTISVR 350

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Job time: 57 secs

Tue Jan 4 06:38:27 2005

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